

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:39:01 ; Search time 8388.21 Seconds
(without alignments)
11011.138 Million cell updates/sec

Title: US-09-856-681A-1
Perfect score: 3093
Sequence: 1 atgaggtcagaagccttgct.....ccaatgatgcgtgtacataa 3093

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match Length	DB	ID	
	1	3089.8	99.9	6875	11	BC032619 Homo sapi
	2	1439.4	46.5	3226	11	AK042751 Mus muscu
	3	1437.6	46.5	3329	11	AK082711 Mus muscu
	4	1065.8	34.5	2411	14	CB605722 AMGNNUC:M
	5	899.4	29.1	1030	12	BM450002 AGENCOURT
	6	896	29.0	1183	12	BM546059 AGENCOURT
	7	828.2	26.8	868	9	AU140366 AU140366
	8	813.8	26.3	891	13	BU186963 AGENCOURT
	9	784.4	25.4	887	12	BG769297 602742838
	10	783.4	25.3	1201	9	AL543344 AL543344
	11	779.4	25.2	848	13	BQ678536 AGENCOURT
	12	772.4	25.0	883	13	BU172225 AGENCOURT
	13	770	24.9	864	13	BQ440312 AGENCOURT
	14	767.4	24.8	874	13	BU838082 AGENCOURT
	15	760.6	24.6	890	13	BQ683009 AGENCOURT
	16	757.4	24.5	953	13	BU854884 AGENCOURT
	17	757	24.5	851	14	CD653925 AGENCOURT
	18	734	23.7	952	13	BU855855 AGENCOURT
	19	713.8	23.1	835	12	BG477592 602522430
	20	698.4	22.6	826	14	CD654452 AGENCOURT
	21	682.2	22.1	4374	11	AK031307 Mus muscu
	22	681.8	22.0	3921	11	AK084922 Mus muscu
	23	680.2	22.0	4476	11	AK052232 Mus muscu
	24	670.2	21.7	716	10	BF970807 602271438
	25	669.4	21.6	802	14	CD653501 AGENCOURT
	26	668.4	21.6	805	14	CD656935 AGENCOURT
	27	667	21.6	890	13	BU856543 AGENCOURT
	28	664.8	21.5	736	10	BE277845 601120064
	29	660.4	21.4	794	10	AW954605 EST366675
	30	656.2	21.2	823	12	BG327694 602426690
	31	645.8	20.9	651	9	AL602452 DKFZp686M
	32	636.6	20.6	643	10	BE408781 601303483
	33	631.8	20.4	685	10	BE265000 601193829
	34	629.8	20.4	703	10	BE384511 601277886
	35	615.2	19.9	926	12	BG326467 602425312
	36	614.4	19.9	746	13	BQ770491 UI-M-FI0-
	37	614.4	19.9	795	14	CB245479 UI-M-FY0-
	38	612.2	19.8	772	13	BQ425051 AGENCOURT
	39	611.8	19.8	895	12	BI819955 603035314
	40	608.8	19.7	777	13	BU708565 UI-M-FI0-
	41	608.6	19.7	747	14	CF535602 UI-M-GH0-
	42	604.4	19.5	771	14	CA513024 UI-R-FJ0-
	43	589.6	19.1	829	12	BI824613 603033546
	44	589.2	19.0	690	12	BG333712 602460715
c	45	588.8	19.0	592	14	CA337090 NISC lv09

ALIGNMENTS

RESULT 1

BC032619

LOCUS BC032619 6875 bp mRNA linear HTC 04-MAR-2003

DEFINITION Homo sapiens, similar to sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:5578066, mRNA.

ACCESSION BC032619

VERSION BC032619.1 GI:22749800

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 6875)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 69 Row: 0 Column: 4

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 11991659

This clone has the following problem: retained intron.

FEATURES

source

Location/Qualifiers

1. .6875

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5578066"

/tissue_type="Skin, melanotic melanoma."

/clone_lib="NIH_MGC_72"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 99.9%; Score 3089.8; DB 11; Length 6875;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3091; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      792 ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC 851

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      852 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 911

Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     912 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 971

Qy     181 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTTACTGTTGAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     972 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTTACTGTTGAT 1031

Qy     241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
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Db    1032 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 1091

Qy     301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 360
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Db    1092 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 1151

Qy     361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
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Db    1152 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 1211

Qy     421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Db    1212 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 1271

Qy     481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Db    1272 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 1331

Qy     541 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Db    1332 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 1391

Qy     601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA 660
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Db    1392 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA 1451

Qy     661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1452 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 1511
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Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	780
Db	1512	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	1571
Qy	781	GATATGGGAGGATCTCAAAGAGTCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	1572	GATATGGGAGGATCTCAAAGAGTCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	1631
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	900
Db	1632	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	1691
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1692	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1751
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1752	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1811
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1812	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1871
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCTCCTTAGAAAGATATGCAACC	1140
Db	1872	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCTCCTTAGAAAGATATGCAACC	1931
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1932	TCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACCCGCTCATGGATGAG	1991
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1992	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	2051
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	2052	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	2111
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	2112	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	2171
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTACAACCTTGAAAAATGCAGCTATGAT	1440
Db	2172	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTACAACCTTGAAAAATGCAGCTATGAT	2231
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	2232	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	2291
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	2292	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	2351
Qy	1561	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620

Db	2352	 TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	2411
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	2412	 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	2471
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	2472	 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	2531
Qy	1741	TCCCTCTTGCCCAGCACAACCACATCAGATTGACGCGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	2532	 TCCCTCTTGCCCAGCACAACCACATCAGATTGACGCGCTCAAGAGGGGTATGAGTCTAGG	2591
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2592	 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2651
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA	1920
Db	2652	 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA	2711
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2712	 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	2771
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2772	 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2831
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2832	 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2891
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2892	 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2951
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2952	 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	3011
Qy	2221	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	3012	 ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	3071
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	3072	 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	3131
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCGTGTGATTCCC	2400
Db	3132	 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCGTGTGATTCCC	3191
Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2460

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 Qy 2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCCAG 2520
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 Db 3252 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCCAG 3311
 Qy 2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
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 Db 3312 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 3371
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 Qy 2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
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 Db 3492 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 3551
 Qy 2761 CCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAAC 2820
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 Qy 2821 TCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG 2880
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 Qy 2941 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG 3000
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 Qy 3001 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3060
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 Qy 3061 ACATCCATGAAGCCCAATGATGCGGTGACATAA 3093
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 Db 3852 ACATCCATGAAGCCCAATGATGCGGTGACATAA 3884

RESULT 2

AK042751

LOCUS AK042751 3226 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone:A730020P05 product:sema domain,
 transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A,
 full insert sequence.

ACCESSION AK042751

VERSION AK042751.1 GI:26335300

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3226)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

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ORIGIN

Query Match 46.5%; Score 1439.4; DB 11; Length 3226;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1554; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

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RESULT 3
AK082711

LOCUS AK082711 3329 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230094A19 product:sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, full insert sequence.

ACCESSION AK082711

VERSION AK082711.1 GI:26349884

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3329)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,

Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cdNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match 46.5%; Score 1437.6; DB 11; Length 3329;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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RESULT 4

CB605722

LOCUS CB605722 2411 bp mRNA linear EST 16-MAY-2003

DEFINITION AMGNNUC:MRPE3-00075-D4-WY placenta embryo D17 (10379) Rattus norvegicus cDNA clone mrpe3-00075-d4, mRNA sequence.

ACCESSION CB605722

VERSION CB605722.1 GI:29545334

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 2411)

AUTHORS Amgen EST Program.

TITLE Amgen Rat EST Program

JOURNAL Unpublished (2003)

COMMENT Contact: Dan Fitzpatrick

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00075 row: d column: 4.

FEATURES Location/Qualifiers

source

1. .2411

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="mrpe3-00075-d4"

/tissue_type="placenta embryo"

/clone_lib="placenta embryo D17 (10379)"

/note="Vector: pSPORT1; placenta embryo D17"

ORIGIN

Query Match 34.5%; Score 1065.8; DB 14; Length 2411;

Best Local Similarity 79.5%; Pred. No. 9.6e-242;

Matches 1398; Conservative 0; Mismatches 147; Indels 214; Gaps 3;

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Qy      1338 CATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCT 1397
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11  CGTCTTGAAGTTCTTGGCCAGGATAGGAAGCAGTGGTTTCCTAAATGGCAGCCTTTTCCT 70

Qy      1398 GGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAG 1457
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      71  GGAGGAGATGAATGTTTACAACCCAGAAAAGTGCAGCTATGATGGTGTAGAAGACAAAAG 130

Qy      1458 GATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTG 1517
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      131 GATCATGGGTATGCAGCTCGACAAAGCAAGTGGTTCACCTTTATGTTGCATTCTCTACTTG 190

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Qy	1518	TGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAACCAACCTGTAT	1577
Db	191	TGTGATAAAGGTGCCTCTTGGCCGCTGTGAGCGACATGGGAAGTGTAACCAACCTGTAT	250
Qy	1578	TGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATC	1637
Db	251	CGCCTCCAGAGACCCATATTGTGGGTGGGTAAAGGAACTGGTTCCCTGTGCCCATCTGTC	310
Qy	1638	ACCCAACAGCAGACTGACTTTTGTAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGG	1697
Db	311	ACCCCTTAGCAGACTGGCTTTTGTAGCAAGACATAGAGCGTGGCAATACAGACGGCCTAGG	370
Qy	1698	GGACTGTCACAATTCTTTGTGGCACTGAATGGGCATTCAGTTCCCTCTTGCCAGCAC	1757
Db	371	AGACTGTCACAATTCTTCGTGGCACTGAAT-----	401
Qy	1758	AACCACATCAGATTTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTG	1817
Db	402	-----	401
Qy	1818	GAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCATAA	1877
Db	402	-----	401
Qy	1878	TCACCAAGACAAGAAGGGAGTGATTGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGT	1937
Db	402	-----GGAGTGATTGGGAAAGTTACCTCAAAGCAACGACCAGCTCGT	445
Qy	1938	TCCCGTCACCCCTCTTGGCCATTGCAGTCATCTGGCTTTCGTGCATGGGGGCCGTCTTCTC	1997
Db	446	TCCTGTCACCCCTTTTGGCCATTGCAGTCATTCTGGCTTTTGTGCATGGGGGCAGTCTTCTC	505
Qy	1998	GGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCG	2057
Db	506	CGGCATCATCGTGTATTGTGTGTGTGATCACCGGCGCAAAGACGTGGCGGTAGTGCAACG	565
Qy	2058	CAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAG	2117
Db	566	CAAGGAGAAAGAGCTCACCCACTCGCGTCGGGGATCTATGAGCAGTGTACCAAGCTCAG	625
Qy	2118	CGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACT	2177
Db	626	TGGCCTCTTTGGGGACAGTCAGTCCAAGGACCCAAAGCCTGAGGCCATCCTCACGCCACT	685
Qy	2178	CATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGA	2237
Db	686	CATGCACAATGGCAAACCTGGCCACGCCTAGCAACACCGCCAAGATGCTCATCAAGGCTGA	745
Qy	2238	CCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCA	2297
Db	746	CCAGCATCACTTAGACCTCACCGCCCTGCCCACCCGGAGTCCACCCCAACACTGCAGCA	805
Qy	2298	GAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAAGCTCATCAATGC	2357
Db	806	GAAGCGGAAACCCAACCGGGCAGTCGCGAGTGGGAGAGGAACCAAGCTCATCAATGC	865
Qy	2358	CTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTGCCCCTGCG	2417

Db	866	CTGCACCAAGGACAT-----	880
Qy	2418	GGCCTCCCCCAGCCACATCCCAGCGTGGTGGTCTCTGCCCATCACGCAGCAGGGCTACCA	2477
Db	881	-GCCTCCCCAAGCCACATCCCAGCGTGGTGGTCTCTGCCCATCACACAGCAGGGCTACCA	939
Qy	2478	GCATGAGTACGTGGACCAGCCCCAAATGAGCGA---GGTGGCCCAGATGGCGCTGGAGGA	2534
Db	940	GCACGAATACGTAGATCAGCCCCAAATGAGCGAGGTGGTGGCTCAGATGGCACTGGAGGA	999
Qy	2535	CCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAA	2594
Db	1000	CCAGGCTGCCACCCTGGAGTATAAGACCATCAAAGAGCACCTGAGCAGCAAGAGTCCCAA	1059
Qy	2595	CCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGGGA	2654
Db	1060	CCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGTGA	1119
Qy	2655	GGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGA	2714
Db	1120	GGCCTCTCTGGGTCCCACGGGAGCCTCACTGTCCAGACCGGCCTGAGCAAGCGGCTGGA	1179
Qy	2715	AATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAACCTCGCT	2774
Db	1180	AATGCAACACTCCTCCTCTACGGGCTTGAATATAAGAGGAGCTACCCACGAACCTCGCT	1239
Qy	2775	CACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCTC	2834
Db	1240	CACAAGAAGCCATCAGGCCACCACTCTCAAAAGAAACAATACTAACTCCTCCAATTCTC	1299
Qy	2835	TCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCGCAGAG	2894
Db	1300	CCACCTCTCCAGGAACCAGAGCCTTGGCCGGGGAGACAACCCACCTCCCGCCCGCAGAG	1359
Qy	2895	GGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAG	2954
Db	1360	GGTGGACTCTATCCAGGTGCACAGCCCCAGCCCTCTGGCCAGGCCGTGACTGTTTCGAG	1419
Qy	2955	GCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTC	3014
Db	1420	GCAGCCCAGCCTCAATGCCTACAACCTCACTGACGAGGTCGGGGCTGAAGCGCACCCCTC	1479
Qy	3015	GCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCCTTCCACATCCATGAAGCC	3074
Db	1480	GCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCCCCCTTCCACATCCATGAAGCC	1539
Qy	3075	CAATGATGCGTGTACATAA 3093	
Db	1540	CAATGATGCGTGTACATAA 1558	

BM450002

LOCUS	BM450002	1030 bp	mRNA	linear	EST 05-FEB-2002
DEFINITION	AGENCOURT_6393382 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5528003 5', mRNA sequence.				

ACCESSION BM450002
 VERSION BM450002.1 GI:18499042
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1030)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12204 row: c column: 12
 High quality sequence stop: 733.

FEATURES Location/Qualifiers
 source 1. .1030
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5528003"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 29.1%; Score 899.4; DB 12; Length 1030;
 Best Local Similarity 97.4%; Pred. No. 2.2e-202;
 Matches 956; Conservative 0; Mismatches 19; Indels 7; Gaps 4;

Qy	787	GGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGCTTGAAC	846
Db	1	GGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGCTTGAAC	60
Qy	847	TGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTG	906
Db	61	TGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTG	120
Qy	907	ATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATC	966
Db	121	ATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATC	180
Qy	967	CCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGA	1026
Db	181	CCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGA	240

Qy	1027	TTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCT	1086
Db	241	TTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCT	300
Qy	1087	AAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAAT	1146
Db	301	AAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAAT	360
Qy	1147	GAGTTCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTG	1206
Db	361	GAGTTCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTG	420
Qy	1207	CCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAA	1266
Db	421	CCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAA	480
Qy	1267	ATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCA	1326
Db	481	ATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCA	540
Qy	1327	GAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGAC	1386
Db	541	GAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGAC	600
Qy	1387	AGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTC	1446
Db	601	AGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTC	660
Qy	1447	GAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCG	1506
Db	661	GAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCG	720
Qy	1507	TTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGT-AA	1565
Db	721	TTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAAAGTGT	780
Qy	1566	AAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTG	1625
Db	781	AAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTG	840
Qy	1626	CAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATAC	1685
Db	841	CAGNCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATAC	900
Qy	1686	AGAT-GGTCTGGGGGACTGTCAC--AATTCCTTTGTGGCACTGAA---TGGGCATTCCAG	1739
Db	901	AGATGGGTCTGGGGGAATGTCACCAATTCTTTGTTGGCACTGNAATGGGGCATTTC	960
Qy	1740	TTCCCTCTTGCCCAGCACAACC	1761
Db	961	TTCCCTCTTGCCCAGNACAAAC	982

RESULT 6

BM546059

LOCUS BM546059 1183 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6497880 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588479


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5', mRNA sequence.
ACCESSION   BM546059
VERSION     BM546059.1  GI:18778712
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1183)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12359 row: k column: 08
            High quality sequence stop: 725.

FEATURES             Location/Qualifiers
     source           1. .1183
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5588479"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."

ORIGIN

Query Match          29.0%; Score 896; DB 12; Length 1183;
Best Local Similarity 99.0%; Pred. No. 1.5e-201;
Matches 932; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

Qy    2152 AAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGCGAAGCTCGCCACTCCC GGCAAC 2211
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Db    18 ATGCCGGAGGCCATCCTCACGCCACTCATGCACAACGCGAAGCTCGCCACTCCC GGCAAC 77

Qy    2212 ACGGCCAAGATGCTCATTAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCC ACC 2271
        | |||||||
Db    78 ACGGCCAAGATGCTCATTAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCC ACC 137

Qy    2272 CCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTG G 2331
        | |||||||
Db    138 CCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTG G 197

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Qy	2332	GAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCT	2391
Db	198	GAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCT	257
Qy	2392	GTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTC	2451
Db	258	GTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTC	317
Qy	2452	CTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAG	2511
Db	318	CTGCCCATCACGCAGCAGGGCTACCAGCACGAGTACGTGGACCAGCCCAAATGAGCGAG	377
Qy	2512	GTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAA	2571
Db	378	GTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAA	437
Qy	2572	CATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTG	2631
Db	438	CATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTG	497
Qy	2632	CCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAG	2691
Db	498	CCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAG	557
Qy	2692	ACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAG	2751
Db	558	ACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAG	617
Qy	2752	AGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAAC	2811
Db	618	AGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGNCACCACTCTCAAAGAAAC	677
Qy	2812	AACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGAC	2871
Db	678	AACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGAC	737
Qy	2872	AACCCGCCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCT	2931
Db	738	AACCCGCCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCT	797
Qy	2932	GGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACACTACTGACAAGG	2991
Db	798	GGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACACTACTGACAAAG	857
Qy	2992	TC-GGGGCTGAAGCGTACG-CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTG	3049
Db	858	TCGGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTG	917
Qy	3050	CTCCCCTTTCCACATCCATG-AAGCCCAATGATGCGTGTAC	3089
Db	918	CTCCCCTTTTCACATCCATGAAAGCCCATGATGCGTGTAC	958

RESULT 7
AU140366

LOCUS AU140366 868 bp mRNA linear EST 05-AUG-2002

DEFINITION AU140366 PLACE2 Homo sapiens cDNA clone PLACE2000407 5', mRNA sequence.

ACCESSION AU140366

VERSION AU140366.1 GI:11001887

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 868)

AUTHORS Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y. and Isogai,T.

TITLE HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y., Isogai,T.)

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES Location/Qualifiers

source 1..868
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE2000407"
/tissue_type="placenta"
/clone_lib="PLACE2"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 26.8%; Score 828.2; DB 9; Length 868;
Best Local Similarity 98.3%; Pred. No. 1.7e-185;
Matches 855; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

Qy	368	TTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTCAACCCTT	427
Db	1	TTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTCAACCCTT	60
Qy	428	CCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTACGCGGAATGG	487
Db	61	CCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTACGCGGAATGG	120
Qy	488	CCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGAAACTAT	547
Db	121	CCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGAAACTAT	180
Qy	548	ACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGTCTTGGAG	607
Db	181	ACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGTCTTGGAG	240

Qy 608 AAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCATACTTTG 667
 |||
 Db 241 AAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCATACTTTG 300

Qy 668 TTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCAGTGGAGT 727
 |||
 Db 301 TTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCAGTGGAGT 360

Qy 728 ATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAATGATATGG 787
 |||
 Db 361 ATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAATGATATGG 420

Qy 788 GAGGATCTCAAAGAGTCTTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGCTTGAAC 847
 |||
 Db 421 GAGGATCTCAAAGAGTCTTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGCTTGAAC 480

Qy 848 GCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTGA 907
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 Db 481 GCTCAGTTCCTGGAAACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTGA 540

Qy 908 TTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATCC 967
 |||
 Db 541 TTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATCC 600

Qy 968 CTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGAT 1027
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 Db 601 CTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGAT 660

Qy 1028 TCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCTA 1087
 |||
 Db 661 TCAAGGAACAGAAGTCTNCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCTA 720

Qy 1088 AGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAATG 1147
 |||
 Db 721 AGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTNCTTAGAAAGATATGCAACCTTCAATG 780

Qy 1148 AGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTGC 1207
 |||
 Db 781 AGTTCCCTGATGAT-CCCTGAACTTNATCAAGACGCACCCGTTTCATGGATGA-GCAATGC 838

Qy 1208 CCTCCATCTTCAACAGGCCATGGTTCCTGA 1237
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 Db 839 CCTTCATTTTNAACAGGGCATGGGTNCTGA 868

RESULT 8

BU186963

LOCUS BU186963 891 bp mRNA linear EST 04-SEP-2002

DEFINITION AGENCOURT_7785723 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6138529
 5', mRNA sequence.

ACCESSION BU186963

VERSION BU186963.1 GI:22700947

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE      1 (bases 1 to 891)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: ATCC
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Agencourt Bioscience Corporation
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM13454 row: b column: 02
                High quality sequence stop: 677.

FEATURES             Location/Qualifiers
     source            1..891
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
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                        /clone="IMAGE:6138529"
                        /tissue_type="retinoblastoma"
                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NIH MGC_67"
                        /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                        Average insert size 1.75 kb. Library constructed by Life
                        Technologies."

ORIGIN

Query Match      26.3%; Score 813.8; DB 13; Length 891;
Best Local Similarity 97.3%; Pred. No. 4.5e-182;
Matches 860; Conservative 0; Mismatches 18; Indels 6; Gaps 3;

Qy      946 TCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATT 1005
      || |||||
Db      8 TCCGCACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATT 67

Qy      1006 GCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCA 1065
      |||||
Db      68 GCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCA 127

Qy      1066 GTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTA 1125
      |||||
Db      128 GTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTA 187

Qy      1126 GAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCAC 1185
      |||||
Db      188 GAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCAC 247

Qy      1186 CCGCTCATGGATGAGGCAGTGGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATG 1245
      |||||
Db      248 CCGCTCATGGATGAGGCAGTGGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATG 307

Qy      1246 GTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCAC 1305
      |||||

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Db 308 GTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCAC 367

Qy 1306 ACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGA 1365
 |||

Db 368 ACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGA 427

Qy 1366 AATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAA 1425
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Db 428 AATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAA 487

Qy 1426 AAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCA 1485
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Db 488 AAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCA 547

Qy 1486 AGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGT 1545
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Db 548 AGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGT 607

Qy 1546 GAACGACATGGGAAGTGTAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGG 1605
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Db 608 GAACGACATGGGAAGTGTAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGG 667

Qy 1606 ATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAG 1665
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Db 668 ATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAG 727

Qy 1666 GACATAGAGCGTGGCAATACAGAT-GGTCTGGGGGACTGTCACAATTCCTTTGTGGCACT 1724
 |||

Db 728 GACATAGAGCGTGGCAATACAGATGGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACT 787

Qy 1725 GAATGGGCATTCCAGTTCCTCTTGCCAGCACAAACCACATCAGATTCGACGGCTCAAGA 1784
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Db 788 GAATGGGCATTCCAGTTCCTCTTGCCAGCAC-ACCACATCAGATTCACGGCTCAANGA 846

Qy 1785 GGGGTATGA----GTCTAGGGGAGGAATGCTGGACTGGAAGCAT 1824
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Db 847 AGGGTATGAAGTCCTAAGGGGAGGAAATGCTGGACTGGAAGCAT 890

RESULT 9

BG769297

LOCUS BG769297 887 bp mRNA linear EST 15-MAY-2001

DEFINITION 602742838F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4872704 5', mRNA sequence.

ACCESSION BG769297

VERSION BG769297.1 GI:14079950

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 887)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1749 row: k column: 09
 High quality sequence stop: 862.

FEATURES	Location/Qualifiers
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	/mol_type="mRNA"
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	/clone="IMAGE:4872704"
	/tissue_type="melanotic melanoma, high MDR (cell line)"
	/lab_host="DH10B (phage-resistant)"
	/clone_lib="NIH_MGC_49"
	/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. "

ORIGIN

Query Match 25.4%; Score 784.4; DB 12; Length 887;
 Best Local Similarity 95.8%; Pred. No. 4.4e-175;
 Matches 849; Conservative 0; Mismatches 31; Indels 6; Gaps 4;

Qy	1903	CGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCTCTTGCCATTGCA	1962
Db	2	CGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCTCTTGCCATTGCA	61
Qy	1963	GTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGT	2022
Db	62	GTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGT	121
Qy	2023	GATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCG	2082
Db	122	GATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCG	181
Qy	2083	CGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCC	2142
Db	182	CGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCC	241
Qy	2143	AAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACT	2202
Db	242	AAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACT	301
Qy	2203	CCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCC	2262
Db	302	CCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCC	361

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 2864.r For
 more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI001CF09QP1&cluster=2864.r)
[cgi-bin/cluster.cgi?seq=CS0DI001CF09QP1&cluster=2864.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI001CF09QP1&cluster=2864.r). Contact :
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI001CF09QP1.

FEATURES
 source Location/Qualifiers
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 /clone="CS0DI001YL17"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 25.3%; Score 783.4; DB9; Length 1201;
 Best Local Similarity 96.4%; Pred. No. 9.1e-175;
 Matches 838; Conservative 5; Mismatches 21; Indels 5; Gaps 4;

Qy	1714	TTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCG	1773
Db	221	TTTGTGATGAAACAGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCG	280
Qy	1774	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1833
Db	281	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	340
Qy	1834	TCACCTGACAGCACAGACCCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	1893
Db	341	TCACCTGACAGCACAGACCCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	400
Qy	1894	GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCCTCTTG	1953
Db	401	GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCCTCTTG	460
Qy	1954	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	2013
Db	461	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	520
Qy	2014	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	2073
Db	521	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	580
Qy	2074	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC	2133
Db	581	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC	640
Qy	2134	ACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2193

Db 641 ACTCAATCCAAAGACCCAAAGCCGGAGG-CATCCTCACGCCACTCATGCACAACGGCAAG 699
 Qy 2194 CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGAC 2253
 |||||
 Db 700 CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGAC 759
 Qy 2254 CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC 2313
 |||||
 Db 760 CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC 819
 Qy 2314 CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG 2373
 |||||
 Db 820 CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG 879
 Qy 2374 CCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCTGCGGGCCTCCCCAGCCAC 2433
 |||||
 Db 880 CCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCTGCGGGCCTCCCCAGCCAC 939
 Qy 2434 ATCCCCAGCGTGGTGGTCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC 2493
 |||||
 Db 940 ATCCCCAGCGTGGTGGTCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC 999
 Qy 2494 CAGCCCAAATGAGCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG 2553
 || ||||| :||| :|||
 Db 1000 --AGCCCAAATGAGCGAGGTGG-CCAGATGGCGCTGGARGGCCAGG-CGSCACACTGGAG 1055
 Qy 2554 TATAAGACCATCAAGGAACATCTCAGCAG 2582
 |:||||| : ||| : |||||
 Db 1056 TWTAAGACATCAAGGAAATTYAGCAGCAG 1084

RESULT 11

BQ678536

LOCUS BQ678536 848 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT_8208159 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262572
5', mRNA sequence.

ACCESSION BQ678536

VERSION BQ678536.1 GI:21791215

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 848)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2425 row: b column: 13

High quality sequence stop: 695.

FEATURES
source Location/Qualifiers
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/clone="IMAGE:6262572"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 25.2%; Score 779.4; DB 13; Length 848;
Best Local Similarity 98.1%; Pred. No. 6.6e-174;
Matches 830; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

Qy 1286 CTGGGCCATATCAGAATCACACTGTGGTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 1345
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Db 1 CTGGGCCATATCAGAATCACACTGTGGTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 60

Qy 1346 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 1405
|||||
Db 61 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 120

Qy 1406 TGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 1465
|||||
Db 121 TGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 180

Qy 1466 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 1525
|||||
Db 181 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 240

Qy 1526 AGGTTCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCA 1585
|||||
Db 241 AGGTTCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCA 300

Qy 1586 GAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACA 1645
|||||
Db 301 GAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACA 360

Qy 1646 GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC 1705
|||||
Db 361 GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC 420

Qy 1706 ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACAT 1765
|||||
Db 421 ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACAT 480

Qy 1766 CAGATTGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATC 1825

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Db      481 CAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATC 540
Qy      1826 TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAG 1885
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Db      541 TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAG 600
Qy      1886 ACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCA 1945
      |||
Db      601 ACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCA 660
Qy      1946 CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 2005
      |||
Db      661 CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 720
Qy      2006 CCGTCTACTGCGTCTGTGATCATCGGCGCAAAGA-CGTGGCTGTGGTGCAG-CGCAAGGA 2063
      |||
Db      721 CCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACCGTGGCTGTGGTGCANCCGCAAGGA 780
Qy      2064 GAAGGAGCTCACCCACT-CGCGCCGGGGCTCCATGAG-CAGCGTCACCAAGCTCAGCGGC 2121
      ||
Db      781 AAAAGAGCTCACCCACTCCGCGCGGGGGCTTCATGAGCCAGCGTCACCAAGCTTCACCGG 840
Qy      2122 CTCTTT 2127
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Db      841 CCCTCT 846

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RESULT 12

BU172225

LOCUS BU172225 883 bp mRNA linear EST 04-SEP-2002
 DEFINITION AGENCOURT_7962341 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6106551
 5', mRNA sequence.

ACCESSION BU172225

VERSION BU172225.1 GI:22686209

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 883)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2347 row: m column: 16

High quality sequence stop: 606.

FEATURES Location/Qualifiers

source 1. .883

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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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ORIGIN

```

Query Match          25.0%; Score 772.4; DB 13; Length 883;
Best Local Similarity 98.6%; Pred. No. 3.1e-172;
Matches 779; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy      1301 ATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAA 1360
      || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14  ATTCCACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAA 73

Qy      1361 TAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAAC 1420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74  TAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAAC 133

Qy      1421 CTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACA 1480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      134 CTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACA 193

Qy      1481 GAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCC 1540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      194 GAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCC 253

Qy      1541 GGTGTGAACGACATGGGAAGTGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTG 1600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      254 GGTGTGAACGACATGGGAAGTGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTG 313

Qy      1601 GATGGATAAAGGAAGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTG 1660
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      314 GATGGATAAAGGAAGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTG 373

Qy      1661 AGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGG 1720
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      374 AGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGG 433

Qy      1721 CACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTC 1780
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      434 CACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTC 493

Qy      1781 AAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTG 1840
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      494 AAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTG 553

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Qy 1841 ACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGA 1900
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 Db 554 ACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGA 613

Qy 1901 TTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTG 1960
 |||
 Db 614 TTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTG 673

Qy 1961 CAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCT 2020
 |||
 Db 674 CAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGCTACTGCGTCC 733

Qy 2021 GTGATCATCGGCGCAAAGACGTGGCTGTGGTGACGCGCAAGGAGAAGGAGCTCACCCACT 2080
 |||
 Db 734 GTGATCATCGGCGCAAAAACGTGGCTGTGGTGCCCCGCCAGGAGAAGGAGCTCACCCACT 793

Qy 2081 CGCGCCGGGG 2090
 |||
 Db 794 CGCGCCGGGG 803

RESULT 13

BQ440312

LOCUS BQ440312 864 bp mRNA linear EST 24-MAY-2002

DEFINITION AGENCOURT_7902718 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157758
 5', mRNA sequence.

ACCESSION BQ440312

VERSION BQ440312.1 GI:21179388

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 864)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13504 row: c column: 07

High quality sequence stop: 659.

FEATURES

source

Location/Qualifiers

1. .864

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6157758"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 24.9%; Score 770; DB 13; Length 864;
 Best Local Similarity 96.3%; Pred. No. 1.2e-171;
 Matches 830; Conservative 0; Mismatches 24; Indels 8; Gaps 4;

Qy	1596	TTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGAC	1655
Db	1	TTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGAC	60
Qy	1656	TTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTT	1715
Db	61	TTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTT	120
Qy	1716	TGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCGAC	1775
Db	121	TGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCGAC	180
Qy	1776	GGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTC	1835
Db	181	GGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTC	240
Qy	1836	ACCTGACAGCACAGACCCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGG	1895
Db	241	ACCTGACAGCACAGACCCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGG	300
Qy	1896	AGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGC	1955
Db	301	AGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGC	360
Qy	1956	CATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTG	2015
Db	361	CATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTG	420
Qy	2016	CGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCAC	2075
Db	421	CGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCAC	480
Qy	2076	CCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACAC	2135
Db	481	CCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACAC	540
Qy	2136	TCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCT	2195
Db	541	TCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCT	600
Qy	2196	CGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGACCT	2255
Db	601	CGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGACCT	660
Qy	2256	GACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCG	2315
Db	661	GACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCG	720

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Qy      2316 CGGCAGCCGCG-AGTGGGAGAGGAACCA-GAACCTCATCAATGCCTGCACAAAGGACATG 2373
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Db      721 CGGCAACCGCGAAGTGGGAGAAGAACCANNAACCTCATCAATGCCTGCACAAAGGACATG 780

Qy      2374 CCCCCCATGGG--CTCCCCTGTGATTCCCACGGACCTG---CCCCTGCGGGCCTCCCCC 2427
          ||||||||| ||| ||||| ||||||||| | || |||||||||
Db      781 CCCCCCATGGGGCTCCCCTGNTGATTTCCACGGACCCGTGCCCTGNCGGGGCCTCCCCC 840

Qy      2428 AGCCACATCCCCAGCGTGGTGG 2449
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Db      841 AGCACAATCNCCCCCAAGGGGG 862

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NIH_MGC Library."

ORIGIN

Query Match 24.8%; Score 767.4; DB 13; Length 874;
 Best Local Similarity 99.2%; Pred. No. 4.8e-171;
 Matches 771; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1286 CTGGGCCATATCAGAATCACACTGTGGTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 1345
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 Db 1 CTGGGCCATATCAGAATCACACTGTGGTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 60

Qy 1346 AGTTTTTGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 1405
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 Db 61 AGTTTTTGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 120

Qy 1406 TGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 1465
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 Db 121 TGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 180

Qy 1466 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 1525
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 Db 181 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 240

Qy 1526 AGGTTCCCTTGCCGGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCA 1585
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 Db 241 AGGTTCCCTTGCCGGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCA 300

Qy 1586 GAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACA 1645
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 Db 301 GAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACA 360

Qy 1646 GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC 1705
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 Db 361 GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC 420

Qy 1706 ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACAT 1765
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 Db 421 ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACAT 480

Qy 1766 CAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATC 1825
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 Db 481 CAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATC 540

Qy 1826 TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAG 1885
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 Db 541 TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAG 600

Qy 1886 ACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCTGTC 1945
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 Db 601 ACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCTGTC 660

Qy 1946 CCCTCTTGCCATTGCAGTCATCCTGGCTTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 2005
 |||||
 Db 661 CCCTCTTGCCATTGCAGTCATCCTGGCTTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 720

Qy 2006 CCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGG 2062
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Db 721 CCGTCTACTGCGTCTGTGATCATCGGCGCCAAGACGTGGCTGTGGTGCCACGCCAAG 777

RESULT 15

BQ683009

LOCUS BQ683009 890 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT_8208014 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262587 5', mRNA sequence.

ACCESSION BQ683009

VERSION BQ683009.1 GI:21795688

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 890)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2425 row: c column: 04

High quality sequence stop: 621.

FEATURES

source

Location/Qualifiers

1. .890

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6262587"

/tissue_type="melanotic melanoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_112"

/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 24.6%; Score 760.6; DB 13; Length 890;

Best Local Similarity 97.0%; Pred. No. 2e-169;

Matches 808; Conservative 0; Mismatches 19; Indels 6; Gaps 3;

Qy 1286 CTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 1345

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Db 1 CTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 60

Qy	1346	AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA	1405
Db	61	AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA	120
Qy	1406	TGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG	1465
Db	121	TGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG	180
Qy	1466	GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA	1525
Db	181	GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA	240
Qy	1526	AGGTTCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCA	1585
Db	241	AGGTTCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCA	300
Qy	1586	GAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACA	1645
Db	301	GAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACA	360
Qy	1646	GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC	1705
Db	361	GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC	420
Qy	1706	ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACAT	1765
Db	421	ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACAT	480
Qy	1766	CAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATC	1825
Db	481	CAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATC	540
Qy	1826	TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCATAATCACCAAG	1885
Db	541	TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCATAATCACCAAG	600
Qy	1886	ACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCA	1945
Db	601	ACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCA	660
Qy	1946	CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCCTCTTCTCGGGCATCA	2005
Db	661	CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCCTCTTCTCGGGCATCA	720
Qy	2006	CCGTCTACTGCGTCTGTGATCATCGGCGCAAAG-ACGTGGCTGTGGTGCAGCGCAAGG--	2062
Db	721	CCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAACGTGGCTGTGGGGCACCGCAAGGGA	780
Qy	2063	--AGAAGGAGCTACCCACTCGCGCCGGGGCTCCA-TGAGCAGCGTCACCAAG	2112
Db	781	GAAGGAGCTTACCCATTCCCGCCGGGGCTCCATTGAGAGGCGTCACCAAG	833

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Job time : 8396.21 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 21:56:51 ; Search time 12300 Seconds
(without alignments)
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Title: US-09-856-681A-1
Perfect score: 3093
Sequence: 1 atgaggtcagaagccttgct.....ccaatgatgcgtgtacataa 3093

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 35: em_htg_rod:*
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 39: em_htgo_hum:*
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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	3093	100.0		3093	6	AX026741	AX026741 Sequence
2	3093	100.0		3862	6	AX026746	AX026746 Sequence
3	3093	100.0		3862	9	AF279656	AF279656 Homo sapi
4	3038	98.2		3498	6	BD274938	BD274938 POLYNUCLE
5	3032	98.0		4250	9	AB037789	AB037789 Homo sapi
6	2975	96.2		4982	6	AX780545	AX780545 Sequence
7	2969.6	96.0		6060	6	AX884099	AX884099 Sequence
8	2969.6	96.0		6060	6	BD160721	BD160721 Primer fo
9	2969.6	96.0		6060	9	AK027867	AK027867 Homo sapi
10	2746.2	88.8		3550	6	AX099520	AX099520 Sequence
11	2746.2	88.8		3550	6	BD190797	BD190797 Secreted
12	2698	87.2		3333	6	BD274939	BD274939 POLYNUCLE
13	2584	83.5		4702	10	BC059238	BC059238 Mus muscu
14	2414.8	78.1		3018	10	AF288666	AF288666 Mus muscu
15	2282.4	73.8		4139	10	BC062979	BC062979 Mus muscu
16	2182.4	70.6		3041	6	AX882248	AX882248 Sequence
17	2182.4	70.6		3041	6	BD159617	BD159617 Primer fo
18	2182.4	70.6		3041	9	AK027501	AK027501 Homo sapi
19	2137.4	69.1		2770	10	AF030430	AF030430 Mus muscu
20	1881.6	60.8		1890	6	BD274951	BD274951 POLYNUCLE
21	1824.4	59.0		2293	6	AX879422	AX879422 Sequence
22	1824.4	59.0		2293	6	BD157826	BD157826 Primer fo
23	1824.4	59.0		2293	9	AK027471	AK027471 Homo sapi
24	1742.4	56.3		2227	6	BD127394	BD127394 Primer fo
25	1742.4	56.3		2227	9	AK074975	AK074975 Homo sapi
26	1666.4	53.9		2306	6	AX882662	AX882662 Sequence
27	1666.4	53.9		2306	6	BD159853	BD159853 Primer fo
28	1666.4	53.9		2306	9	AK027654	AK027654 Homo sapi
29	1462	47.3		2123	6	AX876167	AX876167 Sequence
30	1462	47.3		2123	6	BD155987	BD155987 Primer fo
31	1462	47.3		2123	9	AK027439	AK027439 Homo sapi
32	1367.2	44.2		3634	9	AK096337	AK096337 Homo sapi
33	1200	38.8	131823	2		AC010497	AC010497 Homo sapi

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	35	1200	38.8	154061	9	AC008524	AC008524 Homo sapi
	36	1200	38.8	179647	2	AC108124	AC108124 Homo sapi
c	37	1200	38.8	188207	2	AC010233	AC010233 Homo sapi
	38	1122	36.3	4350	5	BC061707	BC061707 Danio rer
	39	1023.8	33.1	169529	10	AC124466	AC124466 Mus muscu
c	40	1023.8	33.1	170386	2	AC124181	AC124181 Mus muscu
	41	1023.8	33.1	184366	10	AC121783	AC121783 Mus muscu
	42	1023.8	33.1	237974	2	AC094771	AC094771 Rattus no
c	43	1023.8	33.1	253924	2	AC126707	AC126707 Rattus no
	44	1023.8	33.1	258786	2	AC125773	AC125773 Rattus no
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ALIGNMENTS

RESULT 1

AX026741

LOCUS AX026741 3093 bp DNA linear PAT 16-SEP-2000

DEFINITION Sequence 1 from Patent WO0031252.

ACCESSION AX026741

VERSION AX026741.1 GI:10187886

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Klostermann, A. and Behl, C.

TITLE Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target

JOURNAL Patent: WO 0031252-A 1 02-JUN-2000;

KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN (DE)

FEATURES Location/Qualifiers

source

1. .3093

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/mol_type="unassigned DNA"

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CDS

1. .3093

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ORIGIN

Query Match 100.0%; Score 3093; DB 6; Length 3093;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3093; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC	60
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Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	120
Db	61	CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	120
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Qy	181	ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	181	ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT	360
Db	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT	360
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTGTCTGTGGAACATAATGCCTTC	420
Db	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTGTCTGTGGAACATAATGCCTTC	420
Qy	421	AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	421	AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660

Db	601	CTTGGAGAAAAGCCCTACCCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	840
Db	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	840
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGT'TTTTACT	1020
Db	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGT'TTTTACT	1020
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
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Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGT'TTACAACCTCTGAAAAATGCAGCTATGAT	1440
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Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
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Qy	1561	TGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1561	TGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGTAGCAGGACATAGAGCGTGGC	1680
Db	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGTAGCAGGACATAGAGCGTGGC	1680
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
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Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAA	1920
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Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
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Db	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
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Db	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
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Db	2161	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Qy	2221	ATGCTCATTAAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
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Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGAGCCGCGAGTGGGAGAGGAAC	2340
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Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
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Db	2401	ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATC	2460
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCAG	2520
Db	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCAG	2520
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
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Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2760
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Qy	2761	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC	2820
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Qy	2821	TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2880
Db	2821	TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2880
Qy	2881	CCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	2940
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Qy	2941	GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG	3000
Db	2941	GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG	3000
Qy	3001	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC	3060
Db	3001	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC	3060
Qy	3061	ACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3061	ACATCCATGAAGCCCAATGATGCGTGTACATAA	3093

RESULT 2

AX026746

LOCUS AX026746 3862 bp DNA linear PAT 16-SEP-2000

DEFINITION Sequence 6 from Patent WO0031252.

ACCESSION AX026746
 VERSION AX026746.1 GI:10187890
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Klostermann,A. and Behl,C.
 TITLE Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal
 development and regeneration mechanisms during apoptosis, and its
 use as a potential drug target
 JOURNAL Patent: WO 0031252-A 6 02-JUN-2000;
 KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL
 CHRISTIAN (DE)
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ORIGIN

Query Match 100.0%; Score 3093; DB 6; Length 3862;
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 Matches 3093; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	120

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Db	1078	AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	1137
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGAGATGGA	540
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Db	1318	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	1377
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Db	1378	GTGGAGTATAACACCATGGGAAAGGTAGTTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAT	1437
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	840
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Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1978	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	2037
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Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
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Qy	1741	TCCCTCTTGCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
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RESULT 3

AF279656

LOCUS AF279656 3862 bp mRNA linear PRI 11-DEC-2000

DEFINITION Homo sapiens semaphorin SEMA6A1 mRNA, complete cds.

ACCESSION AF279656

VERSION AF279656.1 GI:11093650

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3862)

AUTHORS Klostermann,A., Lutz,B., Gertler,F. and Behl,C.

TITLE The orthologous human and murine semaphorin 6A-1 proteins
(SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
zyxin-like domain

JOURNAL J. Biol. Chem. 275 (50), 39647-39653 (2000)

MEDLINE 20564339

PUBMED 10993894

REFERENCE 2 (bases 1 to 3862)

AUTHORS Klostermann,A., Lutz,B., Gertler,F. and Behl,C.

TITLE Direct Submission

JOURNAL Submitted (19-JUN-2000) Independent Research Group

Neurodegeneration, MPI of Psychiatry, Kraepelinstrasse 2-10, Munich

80804, Germany

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 3093; DB 9; Length 3862;
Best Local Similarity 100.0%; Pred. No. 0;
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Qy 241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
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Db 898 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 957

Qy 301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 360
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Db 1078 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 1137

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Db	1918	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1977
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1978	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	2037
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTCACAACTCTGAAAAATGCAGCTATGAT	1440
Db	2038	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTCACAACTCTGAAAAATGCAGCTATGAT	2097
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
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Db	2218	TGTAACAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	2277
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Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	2338	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	2397
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Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2520
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Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
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RESULT 4

BD274938

LOCUS BD274938 3498 bp DNA linear PAT 17-JUL-2003

DEFINITION POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY.

ACCESSION BD274938

VERSION BD274938.1 GI:33084706

KEYWORDS JP 2002538786-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3498)

AUTHORS Shimkets,R.A.

TITLE POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY

JOURNAL Patent: JP 2002538786-A 2 19-NOV-2002;

CuraGen Corporation,Richard A Shimkets

COMMENT OS Homo sapiens

PN JP 2002538786-A/2

PD 19-NOV-2002

PF 09-MAR-2000 JP 2000603363

PR 08-MAR-2000 US 09/520781,09-MAR-1999 US 60/123667 PI

richard a shimkets

CC

FH Key Location/Qualifiers

FT CDS (214)..(3030)

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FEATURES Location/Qualifiers

source 1..3498

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Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db     334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy     181 ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db     514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAAACATAAGGATGAGTGCCACAACCTT 573

Qy     361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTGTCTGTGGAACATAATGCCTTC 420
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Qy     601 CTTGGAGAAAGCCCTACCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA 660
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Qy     661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTCAGGGAAATAGCA 720
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Db     874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTCAGGGAAATAGCA 933

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Db     934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy     781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC 840
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Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
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Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCTGAGAACAATGGTCAGATACCGCCTT	1260
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Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
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Db	1774	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
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Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
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RESULT 5
AB037789

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VERSION    AB037789.1  GI:7243116
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SOURCE     Homo sapiens (human)
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REFERENCE  1  (sites)
AUTHORS    Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O.
TITLE      Prediction of the coding sequences of unidentified human genes.
            XVI. The complete sequences of 150 new cDNA clones from brain which
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JOURNAL    DNA Res. 7 (1), 65-73 (2000)

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MEDLINE 20181126
 PUBMED 10718198
 REFERENCE 2 (bases 1 to 4250)
 AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
 TITLE Direct Submission
 JOURNAL Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)

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ORIGIN

Query Match 98.0%; Score 3032; DB 9; Length 4250;
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Db	1870	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1929
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AX780545

LOCUS AX780545 4982 bp DNA linear PAT 14-JUL-2003

DEFINITION Sequence 2702 from Patent WO03039443.

ACCESSION AX780545

VERSION AX780545.1 GI:32697539

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S., Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.

TITLE Novel genetic markers for leukemias

JOURNAL Patent: WO 03039443-A 2702 15-MAY-2003;

Deutsches Krebsforschungszentrum (DE) ;

Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,

PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)

FEATURES Location/Qualifiers

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ORIGIN

Query Match 96.2%; Score 2975; DB 6; Length 4982;
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Qy     421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Qy     481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1092 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 1151

Qy     541 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Db    1152 AAATATACTCAGCCNCAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 1211

Qy     601 CTTGG-AGAAAGCCCTACCCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACC 659
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Db    1212 CTTGGNAGAAAGCCCTACCCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACC 1271

Qy     660 ATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGC 719
        ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1272 ATACTTNGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGC 1331
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Qy	720	AGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAA	779
Db	1332	AGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAA	1391
Qy	780	TGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCG	839
Db	1392	TGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCG	1451
Qy	840	CTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTAC	899
Db	1452	CTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTAC	1511
Qy	900	AGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAA	959
Db	1512	AGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAA	1571
Qy	960	CAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTAC	1019
Db	1572	CAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTAC	1631
Qy	1020	TGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACG	1079
Db	1632	TGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACG	1691
Qy	1080	AGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAAC	1139
Db	1692	AGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAAC	1751
Qy	1140	CTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGA	1199
Db	1752	CTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGA	1811
Qy	1200	GGCAGTGGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCT	1259
Db	1812	GGCAGTGGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCT	1871
Qy	1260	TACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCT	1319
Db	1872	TACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCT	1931
Qy	1320	GGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTTCT	1379
Db	1932	GGGATCAGAGAAGGGAATCATCTTGAAGTTTTTNGGCCAGAATAGGAAATAGTGGTTTTTCT	1991
Qy	1380	AAATGACAGCCTTTTCCTGGAGGAGATG-AGTGTTTACAACCTCTGAAAAATGCAGCTATG	1438
Db	1992	AAATGACAGCCTTTTCCTGGAGGAGATGNAGTGTTTACAACCTCTGAAAAATGCAGCTATG	2051
Qy	1439	ATGGAGTCGAAGACAAAAGGATCATGGGCATG-CAGCTGGACAGAGCAAGCAGCTCTCTG	1497
Db	2052	ATGGAGTCGAAGACAAAAGGATCATGGGCATGNCAGCTGGACAGAGCAAGCAGCTCTCTG	2111
Qy	1498	TATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTG-GCCGGTGTGAACGACATGG	1556
Db	2112	TATGTTGCGTNCTCTACCTGTGTGATAAAGGTTCCCCTTGNGCNGGTGTGAACGACATGG	2171

Qy	1557	GAAGTGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGG	1616
Db	2172	GAAGTGTAAAAANCCGTGTATTGCNNCCAGAGACCCATATTGTGGATGGATAAAGGANGG	2231
Qy	1617	TGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCG	1676
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Qy	1677	TGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	2292	TGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTTC	2351
Qy	1727	-----ATGGGCATTCCAGTTCCT	1745
Db	2352	AACTCCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCT	2411
Qy	1746	CTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGG	1805
Db	2412	CTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGG	2471
Qy	1806	AATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGT	1865
Db	2472	AATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGT	2531
Qy	1866	GTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCA	1925
Db	2532	GTCTTCCCATAAATCACNAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCA	2591
Qy	1926	CGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTTCGTCATGGG	1985
Db	2592	CGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTTCGTCATGGG	2651
Qy	1986	GGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGC	2045
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Qy	2046	TGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGT	2105
Db	2712	TGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGT	2771
Qy	2106	CACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGAGGCCAT	2165
Db	2772	CACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGAGGCCAT	2831
Qy	2166	CCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCT	2225
Db	2832	CCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCT	2891
Qy	2226	CATTAAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCC	2285
Db	2892	CATTAAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCC	2951
Qy	2286	AACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAA	2345
Db	2952	AACGCTGCAGCAGAAGCGGAANCCAGCCGCGGCANCCGCGAGTGGGAGAGGAACCAGAA	3011
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Db	3012	 CCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGA	3071
Qy	2406	CCTGCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCA	2465
Db	3072	 CCTGCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCA	3131
Qy	2466	GCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCAGATGGC	2525
Db	3132	 GCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCAGATGGC	3191
Qy	2526	GCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAA	2585
Db	3192	 GCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAA	3251
Qy	2586	GAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCC	2645
Db	3252	 GAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCC	3311
Qy	2646	ACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAA	2705
Db	3312	 ACAGCGGGAGGCNTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAA	3371
Qy	2706	GCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCAC	2765
Db	3372	 GCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCAC	3431
Qy	2766	GAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTC	2825
Db	3432	 GAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTC	3491
Qy	2826	CAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGC	2885
Db	3492	 CAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGC	3551
Qy	2886	CCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGAC	2945
Db	3552	 CCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGAC	3611
Qy	2946	TGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTGCGGGCTGAAGCG	3005
Db	3612	 TGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTGCGGGCTGAAGCG	3671
Qy	3006	TACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATC	3065
Db	3672	 TACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATC	3731
Qy	3066	CATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3732	 CATGAAGCCCAATGATGCGTGTACATAA	3759

RESULT 7

AX884099

LOCUS	AX884099	6060 bp	DNA	linear	PAT 17-DEC-2003
DEFINITION	Sequence 19004 from Patent EP1074617.				
ACCESSION	AX884099				

VERSION AX884099.1 GI:40039000
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
 Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primers for synthesising full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 19004 07-FEB-2001;
 Research Association for Biotechnology (JP)
 FEATURES Location/Qualifiers
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 CDS 89. .1345
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ORIGIN

Query Match 96.0%; Score 2969.6; DB 6; Length 6060;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2994; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy 96 CAACTATACAAAACAGTATCCGGTGTGTTGTGGGCCACAAGCCAGGACGGAACACCACACA 155
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 Db 1 CAACTATACAAAACAGTATCCGGTGTGTTGTGGGCCACAAGCCAGGACGGAACACCACACA 60
 Qy 156 GAGGCACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGC 215
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GAGGCACAGGCTGGACATCCAGGTGATTATGATCATGAACGGAACCCCTCTACATTGCTGC 120
 Qy 216 TAGGGACCATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAG 275
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 Db 121 TAGGGACCATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAG 180
 Qy 276 CAAAAAAGTACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA 335
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 Db 181 CAAAAAAGTACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA 240
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 Db 241 ACATAAGGATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATT 300
 Qy 396 GTTGTCTGTGGAACATAATGCCTTCAACCCCTCCTGCAGAACTATAAGATGGATACATT 455

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Db	361	 GGAACCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC	420
Qy	516	CAACGTTGCACTGTTTGCAGATGGAAAAC TATACTCAGCCACAGTGACTGACTTCCTTGC	575
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Qy	576	CATTGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCA	635
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Qy	636	CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT	695
Db	541	 CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT	600
Qy	696	CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCT	755
Db	601	 CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCT	660
Qy	756	AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAAACA	815
Db	661	 AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAAACA	720
Qy	816	GTGGACGTCGTTCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTA	875
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Qy	876	TTTCAACATTCTCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCT	935
Db	781	 TTTCAACATTCTCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCT	840
Qy	936	GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT	995
Db	841	 GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT	900
Qy	996	GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC	1055
Db	901	 GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC	960
Qy	1056	CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC	1115
Db	961	 CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC	1020
Qy	1116	ATCCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCAT	1175
Db	1021	 ATCCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCAT	1080
Qy	1176	CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTTCCT	1235
Db	1081	 CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTTCCT	1140
Qy	1236	GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA	1295

Db	1141	GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA	1200
Qy	1296	TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC	1355
Db	1201	TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC	1260
Qy	1356	CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA	1415
Db	1261	CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA	1320
Qy	1416	CAACTCTG-AAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC	1474
Db	1321	CAACTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC	1380
Qy	1475	TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC	1534
Db	1381	TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC	1440
Qy	1535	TTGGCCGGTGTGAACGACATGGGAAGTGT-AAAAAAACCTGTATTGCCTCCAGAGACCCA	1593
Db	1441	TTGGCCGGTGTGAACGACATGGGAAGTGTAaaaaaacctgtattgcctccagagaccca	1500
Qy	1594	TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG	1653
Db	1501	TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG	1560
Qy	1654	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1713
Db	1561	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1620
Qy	1714	TTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCTG	1773
Db	1621	TTTGTGGCACTGAATGGGCATTCTAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCTG	1680
Qy	1774	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1833
Db	1681	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1740
Qy	1834	TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAAATCACCAAGACAAGAAG	1893
Db	1741	TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAAATCACCAAGACAAGAAG	1800
Qy	1894	GGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG	1953
Db	1801	GGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG	1860
Qy	1954	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	2013
Db	1861	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	1920
Qy	2014	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	2073
Db	1921	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	1980
Qy	2074	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCCTTTGGGGAC	2133
Db	1981	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCCTTTGGGGAC	2040

Qy	2134	ACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2193
Db	2041	ACTCAATCCGAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2100
Qy	2194	CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTTAAAGCAGACCAGCACCTGGAC	2253
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Qy	2254	CTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC	2313
Db	2161	CTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC	2220
Qy	2314	CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG	2373
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Qy	2374	CCCCCATGGGCTCCCCTGTGATTCCACGGACCTGCCCCTGCGGGCCTCCCCAGCCAC	2433
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Qy	2434	ATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC	2493
Db	2341	ATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC	2400
Qy	2494	CAGCCCAAAATGAGCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG	2553
Db	2401	CAGCCCAAAATGAGCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG	2460
Qy	2554	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2613
Db	2461	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2520
Qy	2614	GAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCG	2673
Db	2521	GAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCG	2580
Qy	2674	GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC	2733
Db	2581	GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC	2640
Qy	2734	TACGGGGTTGACTATAAGAGGAGCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCC	2793
Db	2641	TACGGGGTTGACTATAAGAGGAGCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCC	2700
Qy	2794	ACCACTCTCAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG	2853
Db	2701	ACCACTCTCAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG	2760
Qy	2854	AGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTG	2913
Db	2761	AGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTG	2820
Qy	2914	CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCC	2973
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RESULT 8

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BD160721
LOCUS      BD160721                      6060 bp    DNA        linear    PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION  BD160721
VERSION    BD160721.1  GI:27866479
KEYWORDS   JP 2002191363-A/15564.
SOURCE     Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 6060)
  AUTHORS  Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE    Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 15564 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT    OS  Homo sapiens (human)
            PN  JP 2002191363-A/15564
            PD  09-JUL-2002
            PF  28-JUL-2000 JP 2000280990
            PI  TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI  SAITO,
            PI  JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI  KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
            10,
            PC  C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
            Primer for synthesizing full-length cDNA and use thereof FH  Key
            Location/Qualifiers
            FT  CDS (89)..(1342).
FEATURES   Location/Qualifiers
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ORIGIN

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Query Match      96.0%;  Score 2969.6;  DB 6;  Length 6060;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 2994;  Conservative 0;  Mismatches 4;  Indels 2;  Gaps 2;

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Db      1  CAACTATACAAAACAGTATCCGGTGTGTTGTGGGCCACAAGCCAGGACGGAACACCACACA 60

Qy      156 GAGGCACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGC 215

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Db	61	 GAGGCACAGGCTGGACATCCAGGTGATTATGATCATGAACGGAACCCCTCTACATTGCTGC	120
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Db	121	 TAGGGACCATATTTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAG	180
Qy	276	CAAAAAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA	335
Db	181	 CAAAAAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA	240
Qy	336	ACATAAGGATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATT	395
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Qy	396	GTTTGTCTGTGGAACATAATGCCTTCAACCCCTCCTGCAGAACTATAAGATGGATACATT	455
Db	301	 GTTTGTCTGTGGAACATAATGCCTTCAACCCCTCCTGCAGAACTATAAGATGGATACATT	360
Qy	456	GGAACCATTTCGGGGATGAATTGAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC	515
Db	361	 GGAACCATTTCGGGGATGAATTGAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC	420
Qy	516	CAACGTTGCACTGTTTGCAGATGGAAACTATACTCAGCCACAGTGACTGACTTCCTTGC	575
Db	421	 CAACGTTGCACTGTTTGCAGATGGAAACTATACTCAGCCACAGTGACTGACTTCCTTGC	480
Qy	576	CATTGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCA	635
Db	481	 CATTGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCA	540
Qy	636	CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT	695
Db	541	 CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT	600
Qy	696	CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTCCC	755
Db	601	 CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTCCC	660
Qy	756	AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA	815
Db	661	 AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA	720
Qy	816	GTGGACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTT	875
Db	721	 GTGGACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTT	780
Qy	876	TTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCT	935
Db	781	 TTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCT	840
Qy	936	GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT	995
Db	841	 GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT	900
Qy	996	GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC	1055

Db	901	GCTTGACATTGCCAGTGT TTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC	960
Qy	1056	CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC	1115
Db	961	CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC	1020
Qy	1116	ATCCTCCTTAGAAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAAC TTCAT	1175
Db	1021	ATCCTCCTTAGAAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAAC TTCAT	1080
Qy	1176	CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT	1235
Db	1081	CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT	1140
Qy	1236	GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA	1295
Db	1141	GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA	1200
Qy	1296	TCAGAATCACACTGTGGT TTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGT TTTTGGC	1355
Db	1201	TCAGAATCACACTGTGGT TTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGT TTTTGGC	1260
Qy	1356	CAGAATAGGAAATAGTGGT TTTTCTAAATGACAGCCT TTTCTGGAGGAGATGAGTGTTTA	1415
Db	1261	CAGAATAGGAAATAGTGGT TTTTCTAAATGACAGCCT TTTCTGGAGGAGATGAGTGTTTA	1320
Qy	1416	CAACTCTG-AAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC	1474
Db	1321	CAACTCTGAAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC	1380
Qy	1475	TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC	1534
Db	1381	TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC	1440
Qy	1535	TTGGCCGGTGTGAACGACATGGGAAGTGT-AAAAAACCTGTATTGCCTCCAGAGACCCA	1593
Db	1441	TTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAACCTGTATTGCCTCCAGAGACCCA	1500
Qy	1594	TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG	1653
Db	1501	TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG	1560
Qy	1654	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1713
Db	1561	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1620
Qy	1714	TTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCTG	1773
Db	1621	TTTGTGGCACTGAATGGGCATTCTAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCTG	1680
Qy	1774	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1833
Db	1681	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1740
Qy	1834	TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	1893
Db	1741	TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	1800

Qy	1894	GGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCTCTTG	1953
Db	1801	GGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCTCTTG	1860
Qy	1954	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	2013
Db	1861	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	1920
Qy	2014	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	2073
Db	1921	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	1980
Qy	2074	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC	2133
Db	1981	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC	2040
Qy	2134	ACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2193
Db	2041	ACTCAATCCGAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2100
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Qy	2254	CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCAGC	2313
Db	2161	CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCAGC	2220
Qy	2314	CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG	2373
Db	2221	CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG	2280
Qy	2374	CCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCCCTGCGGGCCTCCCCAGCCAC	2433
Db	2281	CCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCCCTGCGGGCCTCCCCAGCCAC	2340
Qy	2434	ATCCCCAGCGTGGTGGTCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC	2493
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Qy	2494	CAGCCCCAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG	2553
Db	2401	CAGCCCCAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG	2460
Qy	2554	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2613
Db	2461	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2520
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RESULT 9

AK027867

LOCUS AK027867 6060 bp mRNA linear PRI 01-AUG-2002

DEFINITION Homo sapiens cDNA FLJ14961 fis, clone PLACE4000230, highly similar to Mus musculus semaphorin VIA mRNA.

ACCESSION AK027867

VERSION AK027867.1 GI:14042853

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 6060)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,

University of Tokyo.

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ORIGIN

Query Match 96.0%; Score 2969.6; DB 9; Length 6060;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2994; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Db     61 GAGGCACAGGCTGGACATCCAGGTGATTATGATCATGAACGGAACCCTCTACATTGCTGC 120

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Qy     276 CAAAAAAGTACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA 335
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Qy     336 ACATAAGGATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATT 395
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Qy     456 GGAACCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC 515
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Qy	636	CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT	695
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Qy	696	CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC	755
Db	601	CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC	660
Qy	756	AAGAGTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA	815
Db	661	AAGAGTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA	720
Qy	816	GTGGACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTTA	875
Db	721	GTGGACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTTA	780
Qy	876	TTTCAACATTCTCCAGGCAGTTACAGATGTGATTCTGATCAACGGGCGTGATGTTGTCCCT	935
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Qy	996	GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC	1055
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Qy	1056	CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC	1115
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Db	1141	GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA	1200
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Qy	1356	CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA	1415

Db	1261	 CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA	1320
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Qy	1714	TTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACATCAGATTCCG	1773
Db	1621	 TTTGTGGCACTGAATGGGCATTCTAGTTCCTCTTGCCAGCACAACCACATCAGATTCCG	1680
Qy	1774	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1833
Db	1681	 ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1740
Qy	1834	TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	1893
Db	1741	 TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	1800
Qy	1894	GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG	1953
Db	1801	 GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG	1860
Qy	1954	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	2013
Db	1861	 GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	1920
Qy	2014	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	2073
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Db	2041	 ACTCAATCCGAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2100
Qy	2194	CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCACCTGGAC	2253

Db	2101	CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACTAGCACCACCTGGAC	2160
Qy	2254	CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC	2313
Db	2161	CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC	2220
Qy	2314	CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG	2373
Db	2221	CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG	2280
Qy	2374	CCCCCATGGGCTCCCCTGTGATTCCACGGACCTGCCCCTGCGGGCCTCCCCAGCCAC	2433
Db	2281	CCCCCATGGGCTCCCCTGTGATTCCACGGACCTGCCCCTGCGGGCCTCCCCAGCCAC	2340
Qy	2434	ATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC	2493
Db	2341	ATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC	2400
Qy	2494	CAGCCCCAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCCACTGGAG	2553
Db	2401	CAGCCCCAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCCACTGGAG	2460
Qy	2554	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2613
Db	2461	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2520
Qy	2614	GAGAACCTGGACAGCCTGCCCCCAAAGTTCACAGCGGGAGGCCTCCCTGGGTCCCCCG	2673
Db	2521	GAGAACCTGGACAGCCTGCCCCCAAAGTTCACAGCGGGAGGCCTCCCTGGGTCCCCCG	2580
Qy	2674	GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC	2733
Db	2581	GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC	2640
Qy	2734	TACGGGGTTGACTATAAGAGGAGCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCC	2793
Db	2641	TACGGGGTTGACTATAAGAGGAGCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCC	2700
Qy	2794	ACCACTCTCAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG	2853
Db	2701	ACCACTCTCAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG	2760
Qy	2854	AGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTG	2913
Db	2761	AGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTG	2820
Qy	2914	CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCC	2973
Db	2821	CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCC	2880
Qy	2974	TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC	3033
Db	2881	TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC	2940
Qy	3034	CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGACATAA	3093
Db	2941	CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGACATAA	3000

RESULT 10

AX099520

LOCUS AX099520 3550 bp DNA linear PAT 02-APR-2001

DEFINITION Sequence 160 from Patent WO0119988.

ACCESSION AX099520

VERSION AX099520.1 GI:13538594

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Collins-Racie,L.A., Evans,C.,
Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Agostino,M.J.

TITLE Secreted proteins and polynucleotides encoding them

JOURNAL Patent: WO 0119988-A 160 22-MAR-2001;

Genetics Institute, Inc. (US)

FEATURES

Location/Qualifiers

source

1. .3550

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 88.8%; Score 2746.2; DB 6; Length 3550;

Best Local Similarity 94.5%; Pred. No. 0;

Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db      126 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 185

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG 120
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Db      186 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG 245

Qy      121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db      246 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 305

Qy      181 ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
          |||
Db      306 ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 365

Qy      241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
          |||:|||||
Db      366 ATAGACACATCACACACSGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 425

Qy      301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 360
          |||
Db      426 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 485

Qy      361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 420
          |||
Db      486 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 545

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Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCGGGGATGAATTCAGC	480
Db	546	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCGGGGATGAATTCAGC	605
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	606	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	665
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	666	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	725
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	726	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	785
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	786	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	845
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCTCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	846	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCTCAAGAGTGGCTCAGGTTTGTAAGAAT	905
Qy	781	GATATGGGAGGATCTCAAAGAGTCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	906	GATATGGGAGGATCTCAAAGAGTCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	965
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	966	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1025
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1026	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1085
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1086	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1145
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1146	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1205
Qy	1081	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1206	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1265
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1266	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1325
Qy	1201	GCAGTGGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1326	GCAGTGGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1385

Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1386	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1445
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1446	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1505
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1506	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1565
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1566	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1625
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1626	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1685
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1686	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1745
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1746	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1805
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1806	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT-----	1853
Qy	1741	TCCCTCTTGCCCAGCACAACCACATCAGATTTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
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Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	1854	-----	1853
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAA	1920
Db	1854	-----GGAGTGATTTCGGGAAAGTTACCTCAA	1880
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	1881	GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1940
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	1941	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2000
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2001	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2060
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160

Db	2061	 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2120
Qy	2161	GCCATCCTCAGGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2121	 GCCATCCTCAGGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2180
Qy	2221	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2181	 ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2240
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2241	 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2300
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2301	 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2360
Qy	2401	ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCTCTGCCCATC	2460
Db	2361	 ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCTCTGCCCATC	2420
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2520
Db	2421	 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2480
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2481	 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATTTTCAGC	2540
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2541	 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2600
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2601	 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTTTCAGACCGGTCTA	2660
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2661	 AGCAAGCGGCTGGAAATGCACCACTCCTTTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2720
Qy	2761	CCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC	2820
Db	2721	 CCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC	2780
Qy	2821	TCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2880
Db	2781	 TCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2840
Qy	2881	CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	2940
Db	2841	 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	2900
Qy	2941	GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG	3000

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Qy      3001 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3060
        |||
Db      2961 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3020
Qy      3061 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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Db      3021 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3053

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RESULT 11

BD190797

LOCUS BD190797 3550 bp DNA linear PAT 17-JUL-2003

DEFINITION Secreted proteins and polynucleotides encoding them.

ACCESSION BD190797

VERSION BD190797.1 GI:33000536

KEYWORDS JP 2002514063-A/5.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 3550)

AUTHORS Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
Treacy,M., Spaulding,V. and Agostino,M.J.

TITLE Secreted proteins and polynucleotides encoding them

JOURNAL Patent: JP 2002514063-A 5 14-MAY-2002;
GENETICS INSTITUTE INC Louis O Gerrue,Jonathan M Diver

COMMENT PN JP 2002514063-A/5

PD 14-MAY-2002

PF 17-DEC-1997 JP 1998527963

PR 18-DEC-1996 US 08/769192,13-JAN-1997 US 08/783401 PR
16-DEC-1997 US 08/991872

PI KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
DAVID MERBERG,

PI MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC

C12N15/11,C07K14/47,A61K38/00

CC Strandedness: Double;

CC Topology: Linear;

FH Key Location/Qualifiers.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 88.8%; Score 2746.2; DB 6; Length 3550;

Best Local Similarity 94.5%; Pred. No. 0;

Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db      126 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC 185
Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	246	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	305
Qy	181	ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	306	ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	365
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
		:	
Db	366	ATAGACACATCACACACSGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	425
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	360
Db	426	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	485
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	486	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	545
Qy	421	AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	546	AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	605
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	606	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	665
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	666	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	725
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	726	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	785
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	786	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	845
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	846	GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	905
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	840
Db	906	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	965
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	966	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTATTTCAACATTCTCCAGGCAGTTACA	1025
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTTGGCAACGTTTCTACACCTTATAAC	960
Db	1026	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTTGGCAACGTTTCTACACCTTATAAC	1085

Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1086	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1145
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1146	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1205
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1140
Db	1206	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1265
Qy	1141	TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
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Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1326	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1385
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1386	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1445
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1446	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1505
Qy	1381	AATGACAGCCTTTTCTGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1506	AATGACAGCCTTTTCTGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1565
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1566	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1625
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1626	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1685
Qy	1561	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1686	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1745
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1746	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1805
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1806	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT-----	1853
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1854	-----	1853
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860

Db	1854	-----	1853
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAA	1920
Db	1854	-----GGAGTGATTTCGGGAAAGTTACCTCAAA	1880
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Db	2061	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2120
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2121	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2180
Qy	2221	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2280
Db	2181	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2240
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Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCTGCCCATC	2460
Db	2361	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCTGCCCATC	2420
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Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
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RESULT 12

BD274939

LOCUS BD274939 3333 bp DNA linear PAT 17-JUL-2003

DEFINITION POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY.

ACCESSION BD274939

VERSION BD274939.1 GI:33084707

KEYWORDS JP 2002538786-A/3.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3333)

AUTHORS Shimkets,R.A.

TITLE POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY

JOURNAL Patent: JP 2002538786-A 3 19-NOV-2002;

CuraGen Corporation,Richard A Shimkets

COMMENT OS Homo sapiens

PN JP 2002538786-A/3

PD 19-NOV-2002

PF 09-MAR-2000 JP 2000603363

PR 08-MAR-2000 US 09/520781,09-MAR-1999 US 60/123667 PI

richard a shimkets

CC

FH Key Location/Qualifiers

FT CDS (214)..(2865)

FT misc_feature (2882)

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FT          /note='an n may be any one of a or t or g or
FT          c'.
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Db      514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 573

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Qy      421 AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTTCGGGGATGAATTCAGC 480
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Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAT	780
Db	934	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAT	993
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	994	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	1053
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	900
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Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1114	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1173
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Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
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Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
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Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1593
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Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560

Db	1714	 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAACCAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	 TGTAACCAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT-----	1941
Qy	1741	TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1942	-----	1941
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Qy	1861	GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAAGTTACCTCAAA	1920
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Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCTCTTGGCCATTGCAGTCATCCTGGCTTTTCGTC	1980
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Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2029	 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2088
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Db	2809	CCCACGAACTCGCTCAGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	2868
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RESULT 13

BC059238

LOCUS BC059238 4702 bp mRNA linear ROD 20-OCT-2003

DEFINITION Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, mRNA (cDNA clone MGC:66957 IMAGE:6417475), complete cds.

ACCESSION BC059238
 VERSION BC059238.1 GI:37748386
 KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 4702)
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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 Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 4702)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 125 Row: o Column: 20
 This clone was selected for full length sequencing because it
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Best Local Similarity 89.9%; Pred. No. 0;
Matches 2783; Conservative 0; Mismatches 310; Indels 3; Gaps 1;

Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
      ||| || ||| ||||| ||||| | | ||||| ||||| ||||| |||||
Db      632 ATGCGGCCAGCAGCCTTACTGCTGTGTCTCACACTGCTACACTGCGCTGGGGCTGGTTTC 691

```

Qy 61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
 |||||
 Db 692 CCAGAAGATTCCGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 751

Qy 121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
 |||||
 Db 752 TTTGTGGGCCACAAGCCAGGACGGAACACCACGCAGAGGCACAGGCTGGACATCCAGATG 811

Qy 181 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
 || |||||
 Db 812 ATCATGATCATGAACAGAACCCCTCTACGTTGCTGCTCGAGACCATATTTATACTGTTGAT 871

Qy 241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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 Db 872 ATAGACACATCCACACAGAAGAAATTTACTGTAGCAAAAAACTGACATGGAAATCTAGA 931

Qy 301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 360
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 Db 932 CAGGCTGACGTAGACACATGCAGGATGAAGGGGAAACATAAGGATGAATGTCACAACCTC 991

Qy 361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
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 Db 992 ATTAAAGTTCTTCTCAAGAAGAATGATGATACGCTGTTTGTCTGTGGAACCAATGCCTTC 1051

Qy 421 AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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 Db 1052 AACCCCTTCCTGCAGAAACTACAGGGTCGATACCTTGGAACCTTTTGGGGATGAATTTAGC 1111

Qy 481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
 |||||
 Db 1112 GGAATGGCCAGATGCCCTTATGATGCCAAACATGCCAACATCGCTCTGTTTGCAGATGGA 1171

Qy 541 AAACCTATACTCAGCCACAGTGAAGTGAAGTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
 ||||| ||||| || |||||
 Db 1172 AAACCTATACTCAGCCACAGTGAAGTGAAGTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 1231

Qy 601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCAGGATTCAAAATGGTTGAAAGAACCA 660
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 Db 1232 CTCGGAGACAGCCCTACCCTCAGGACTGTCAAGCATGATTCAAAGTGGTTGAAAGAGCCG 1291

Qy 661 TACTTTGTTCAGCCGTTGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1292 TACTTTGTTCAGCCGTTGATTATGGGACTATATCTACTTCTTCTTCAGAGAAATTGCA 1351

Qy 721 GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAT 780
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 Db 1352 GTAGAATACAACACTATGGGGAAGGTTGTTTCCCTAGGGTGGCTCAGGTTTGTAAAGAAT 1411

Qy 781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC 840
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1412 GACATGGGAGGGTCTCAGAGAGTCCTGGAGAAGCAGTGGACATCTTCTGAAGGCTCGC 1471

Qy 841 TTGAAGTGTCTCAGTTCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1472 CTGAAGTGTCTCGGTGCCTGGAGACTCTCATTTTTATTTCAATATACTCCAGGCAGTTACA 1531

Qy 901 GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC 960

Db	1532	GATGTGATTTCGCATTAATGGCCGTGATGTTGTCTTGGCAACCTTTTCCACACCTTATAAC	1591
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCATGACATGCTTGACATTGCCAGTGTTTTACT	1020
Db	1592	AGCATCCCAGGTTCTGCAGTCTGTGCCATGACATGCTTGACATTGCTAATGTTTTCACT	1651
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1652	GGGAGGTTCAAGGAACAGAAATCACCTGACTCTACCTGGACACCCGTTCCAGACGAACGA	1711
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1712	GTCCCTAAGCCCAGGCCAGGCTGTTGTGCTGGATCATCCTCTTTAGAAAAATATGCAACC	1771
Qy	1141	TCCAATGAGTTCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1772	TCCAATGAGTTTCCCGATGATACCTGAACTTCATTAAGACGCATCCACTCATGGACGAG	1831
Qy	1201	GCAGTGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1832	GCAGTGCCTTCCATCATCAACAGACCTTGGTTCCTGAGAACAATGGTCAGATACCGCCTG	1891
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTCTG	1320
Db	1892	ACCAAAATTGCAGTAGACAACGCTGCCGGGCCATATCAGAATCACACTGTGGTTTTCCTG	1951
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTGTGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1952	GGATCAGAAAAGGGAATCATCCTGAAGTTCCTTGCCAGGATAGGAAGCAGTGGTTCCTA	2011
Qy	1381	AATGACAGCCTTTTCTGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	2012	AATGGCAGCCTTTTCTGAGGAGATGAATGTTTACAACCCAGAAAAGTGCAGCTATGAT	2071
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	2072	GGTGTAGAAGACAAAAGGATCATGGGCATGCAGCTCGACAGAGCGAGTGGCTCACTCTAT	2131
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGTTCCCCTTGCCCGGTGTGAACGACATGGGAAG	1560
Db	2132	GTTGCATTCTCTACTTGTGTGATCAAGGTGCCTCTTGCCCGCTGTGAGCGACATGGGAAG	2191
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	2192	TGTAAAAAACCTGCATCGCCTCCAGAGACCCGATTGTGGGTGGGTAAGGAAAAGTGGT	2251
Qy	1621	GCCTGCAGCCATTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	2252	TCCTGTGCCCATCTGTACCCCTTAGCAGACTGACATTTGAGCAGGACATTGAGCGTGGC	2311
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	2312	AATACGGACGGCTAGGAGACTGTCACAATTCCTTCGTGGCACTGAATGGGCACGCCAGT	2371
Qy	1741	TCCCTCTTGCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800

Db	2372	TCCCTCTATCCCAGCACCACTACGTTCAGATTTCGGCATCCCAGACGGGTATGAGTCTAGG	2431
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2432	GGAGGCATGCTGGACTGGAACGACCTGCTCGAGGCACCTGGCAGCACAGACCCTTTGGGG	2491
Qy	1861	GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAA	1920
Db	2492	GCAGTGTCTCTCATAACCACCAGGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAA	2551
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2552	AGCAACGACCAGCTTGTTCCTGTACCCCTCCTGGCCATTGCAGTCATTCTGGCTTTTGTC	2611
Qy	1981	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2612	ATGGGGGGCCGTCTTCTCGGGCATCATCGTGTATTGTGTGTGCGATCACCGGCGCAAAGAC	2671
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2672	GTGGCAGTAGTGCAGCGCAAGGAGAAAGAGCTCACTCACTCGCGTCGGGGATCTATGAGC	2731
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2732	AGTGTACCAAGCTCAGTGGCCTCTTTGGGGACACCCAGTCCAAGGACCCAAAGCCTGAG	2791
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2792	GCCATCCTCACACCACTCATGCACAACGGCAAGCTGGCCACGCCTAGCAACACCGCCAAG	2851
Qy	2221	ATGCTCATTAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2852	ATGCTCATCAAGGCTGACCAGCATCACCTAGACCTCACCGCCCTGCCACCCAGAGTCC	2911
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2912	ACCCCGACACTGCAGCAGAAACGGAACCCAACCGCGGCAGTCGCGAGTGGGAGAGGAAC	2971
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2972	CAGAACATCATCAATGCCTGCACCAAGGACATGCCTCCCATGGGTTCCCCTGTGATTCCC	3031
Qy	2401	ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	2460
Db	3032	ACGGACCTGCCCCTCCGGGCCTCCCCAAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	3091
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGA---GGTGGCC	2517
Db	3092	ACGCAGCAGGGCTACCAGCACGAGTACGTAGATCAGCCCAAAAATGAGCGAGGTGGTGGCT	3151
Qy	2518	CAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTC	2577
Db	3152	CAGATGGCACTGGAGGACCAGGCTGCCACCCTGGAGTATAAGACCATCAAAGAGCACCTG	3211
Qy	2578	AGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC	2637
Db	3212	AGTAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCT	3271

Qy 2638 AAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGT 2697
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Qy 2698 CTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGC 2757
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 Db 3332 CTGAGCAAGAGGCTGGAGATGCAACACTCCTCCTCTATGGGCTCGAATATAAGAGGAGC 3391

Qy 2758 TACCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACT 2817
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 Db 3392 TACCCACGAACTCGCTCACAAGAAGCCACCAGACCACCACTCTCAAAGAAACAATACT 3451

Qy 2818 AACTCCTCCAATTCCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCG 2877
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 Db 3452 AACTCCTCCAATTCCCTCCACCTCTCCAGGAACCAGAGCTTTGGCCGGGGAGACAACCCA 3511

Qy 2878 CCGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAG 2937
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 Db 3512 CCGCCCGCCCGCAGCGGGTGGACTCTATCCAGGTGCACAGCTCCCAGCCCTCTGGCCAG 3571

Qy 2938 GCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCTGGGG 2997
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 Db 3572 GCCGTGACTGTTTCGAGGCAGCCCAGCCTCAATGCCTACAACCTACTGACGAGGTCTGGGG 3631

Qy 2998 CTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTT 3057
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 Db 3632 CTGAAGCGCACCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCTCCCCTT 3691

Qy 3058 TCCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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 Db 3692 TCCACATCCATGAAGCCCAATGATGCATGTACATAA 3727

RESULT 14

AF288666

LOCUS AF288666 3018 bp mRNA linear ROD 11-DEC-2000

DEFINITION Mus musculus axon guidance signal SEMA6A1 mRNA, complete cds.

ACCESSION AF288666

VERSION AF288666.1 GI:11093908

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3018)

AUTHORS Klostermann,A., Lutz,B., Gertler,F. and Behl,C.

TITLE The orthologous human and murine semaphorin 6A-1 proteins
 (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
 phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
 zyxin-like domain

JOURNAL J. Biol. Chem. 275 (50), 39647-39653 (2000)

MEDLINE 20564339

PUBMED 10993894

REFERENCE 2 (bases 1 to 3018)

AUTHORS Klostermann,A. and Behl,C.

TITLE Direct Submission

JOURNAL Submitted (21-JUL-2000) Independent Research Group
Neurodegeneration, MPI of Psychiatry, Kraepelinstrasse 2-10, Munich
80804, Germany

FEATURES Location/Qualifiers
source 1. .3018
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="brain"
CDS 1. .3018
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ORIGIN

Query Match 78.1%; Score 2414.8; DB 10; Length 3018;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 2703; Conservative 0; Mismatches 312; Indels 81; Gaps 2;

Qy 1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db 1 ATGCGGCCAGCAGCCTTACTGCTGTGCTCACACTGCTACACTGCGCCGGGGCGGGTTTC 60
Qy 61 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG 120
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Db 61 CCAGAAGATTCCGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG 120
Qy 121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db 121 TTTGTGGGCCACAAGCCAGGACGGAACACCACGACAGAGGCACAGGCTGGACATCCAGATG 180
Qy 181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db 181 ATCATGATCATGAACAGAACCCTCTACGTTGCTGCTCGAGACCATATTTATACTGTTGAT 240
Qy 241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
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Db 241 ATAGACACATCCCACACAGAAGAAATTTACTGTAGCAAAAACTGACATGGAAATCTAGA 300

Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGGAAAACATAAGGATGAGTGCCACAACCTTT	360
Db	301		
Qy	361	CAGGCTGACGTAGACACATGCAGGATGAAGGGGAAAACATAAGGATGAATGTCACAACCTTC	360
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	361		
Qy	421	ATTAAAGTTCTTCTCAAGAAGAATGATGATACGCTGTTTGTCTGTGGAACCAATGCCTTC	420
Qy	421	AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTACAGC	480
Db	421		
Qy	481	AACCCCTTCCTGCAGAACTACAGGGTCGATACCTTGAAACTTTTGGGGATGAATTTAGC	480
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	481		
Qy	541	GGAATGGCCAGATGCCCTTATGATGCCAAACATGTCAACATCGCTCTGTTTGCAGATGGA	540
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	541		
Qy	601	AAACTCTACTCGGCTACAGTGACTGACTTTCTGGCCATTGATGCGGTCATTTACAGGAGC	600
Qy	601	CTTGAGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660
Db	601		
Qy	661	CTTGAGAGAAAGCCCTACCCTCAGGACTGTCAAGCATGATTCAAAGTGGTTGAAAGAGCCG	660
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	661		
Qy	721	TACTTTGTCCAAGCCGTGGATTATGGGGACTATATCTACTTCTTCTTCAGAGAAATTGCA	720
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	780
Db	721		
Qy	781	GTAGAATACAACACTATGGGAAAGTTGTTTTCCCTAGGGTGGCTCAGGCTGTAGAAT	780
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	781		
Qy	841	GACATGGGAGGGTCTCAGAGAGTCCTGGAGAAGCAGTGGACATCTTCTGAAGGCTCGC	840
Qy	841	TTGAACTGCTCAGTTCTGAGACTCTCATTTTTATTTC AACATTCTCCAGGCAGTTACA	900
Db	841		
Qy	901	CTGAACTGCTCGGTGCCTGGAGACTCTCATTTTTATTTC AATATACTCCAGGCAGTTACA	900
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTCTACACCTTATAAC	960
Db	901		
Qy	961	GATGTGATTTCGCATTAATGGCCGTGATGTTGTCCTGGCAACCTTTCCACACCTTATAAC	960
Qy	961	AGCATCCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	961		
Qy	1021	AGCATCCCAGGTTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCTGATGTTTTACT	1020
Qy	1021	GGGAGATTCAAGGAACAGAAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1021		
Qy	1081	GGGAGGTTCAAGGAACAGAAATCACCTGACTCTACCTGGACACCCGTTCCAGACGAACGA	1080
Qy	1081	GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1140
Db	1081		
Qy	1140	GTTCCTAAGCCCAGGCCAGGCTGTTGTGCTGGATCATCCTCTTTAGAAAAATATGCAACC	1140
Db	1140		

Qy	1141	TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1141	TCCAATGAGTTCCCGATGATACCCTGAACTTCATTAAGACGCATCCACTCATGGACGAG	1200
Qy	1201	GCAGTGCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1201	GCAGTGCCTTCCATCATCAACAGACCTTGGTTCCTGAGAACAATGGTCAGATACCGCCTG	1260
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1261	ACCAAAATTGCAGTAGACAACGCTGCCGGGCCATATCAGAATCACACTGTGG-----	1312
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1313	-----	1312
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1313	-----TTTCCTGGAGGAGATGAATGTTTACAACCCAGAAAAGTGCAGCTATGAT	1362
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1363	GGTGTAGAAGACAAAAGGATCATGGGCATGCAGCTCGACAGAGCGAGTGGCTCACTCTAT	1422
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1423	GTTGCATTCTCTACTTGTGTGATCAAGGTGCCTCTTGGCCGCTGTGAGCGACATGGGAAG	1482
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1483	TGTAAAAAAACCTGCATCGCCTCCAGAGACCCGTATTGTGGGTGGGTAAGGGAAGGTGGT	1542
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1543	TCCTGTGCCCATCTGTCAACCCCTTAGCAGACTGACATTTGAGCAGGACATTGAGCGTGGC	1602
Qy	1681	AATACAGATGGTCTGGGGGACTGT'CACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1603	AATACGGACGGCCTAGGAGACTGTCACAATTCCTTCGTGGCACTGAATGGGCACGCCAGT	1662
Qy	1741	TCCCTCTTGCCCAACACACATCAGATTTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1663	TCCCTCTATCCCAACACCACTACGTCTAGATTTCGGCATCCCGAGACGGGTATGAGTCTAGG	1722
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	1723	GGAGGCATGCTGGACTGGAACGACCTGCTCGAGGCACCTGGCAGCACAGACCCTTTGGGG	1782
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAA	1920
Db	1783	GCAGTGTCTCTCATAACCACCAGGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAA	1842
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTTCGTC	1980
Db	1843	AGCAACGACCAGCTTGTTCCCTGTCACCCCTCTTGGCCATTGCAGTCATTCTGGCTTTTCGTC	1902
Qy	1981	ATGGGGGGCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040

Db	1903	 ATGGGGGCGCTCTTCTCGGGCATCATCGTGATTGTGTGTGCGATCACCGGCGCAAAGAC	1962
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	1963	 GTGGCAGTAGTGCGGCGCAAGGAGAAAGAGCTCACTCACTCGCGTCGGGGATCTATGAGC	2022
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2023	 AGTGTCTCCGAGCTCAGTGGCCTCTTTGGGGACACCCAGTCCAAGGACCCAAAGCCTGAG	2082
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
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TITLE Direct Submission
 JOURNAL Submitted (26-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
 Web site: <http://genome.uiowa.edu>
 Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
 Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.

 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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33	669	21.6	4234	6	ABA00055	Aba00055	CADHP-2 c
34	661.6	21.4	3205	6	ABS64380	Abs64380	Human sem
35	657.4	21.3	662	4	AAH08370	Aah08370	Human cDN
36	657.4	21.3	1923	4	AAH42598	Aah42598	Partial c
37	657.4	21.3	3694	4	AAH42597	Aah42597	Nucleotid
38	642	20.8	2191	6	ABS64381	Abs64381	Human sem
39	642	20.8	2359	6	ABS64383	Abs64383	Human sem
40	642	20.8	3196	6	ABS64382	Abs64382	Human sem
41	642	20.8	3364	6	ABS64384	Abs64384	Human sem
42	640.6	20.7	889	5	AAS68806	Aas68806	DNA encod
43	577.4	18.7	1896	6	ABS64379	Abs64379	Human sem
44	577.4	18.7	2014	6	AAD38696	Aad38696	Human LP2
45	570.8	18.5	786	4	AAH05233	Aah05233	Human cDN

ALIGNMENTS

RESULT 1

AAD01233

ID AAD01233 standard; DNA; 3862 BP.

XX

AC AAD01233;

XX

DT 04-OCT-2000 (first entry)

XX

DE Human semaphorin 6A-1 cDNA.

XX

KW Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;

KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;

KW gene therapy; diagnostic agent; therapeutic agent; differentiation;

KW cytoskeletal stabilisation; plasticity; ds.

```

XX
OS   Homo sapiens.
XX
FH   Key          Location/Qualifiers
FT   CDS          658..3750
FT               /*tag= a
FT               /product= "Human semaphorin 6A-1"
FT               /note= "This region is specifically claimed as SEQ ID NO:
FT               1 in claim 1"
FT   misc_feature  3532..3747
FT               /*tag= b
FT               /note= "Encodes the binding domain of semaphorin 6A-1
FT               which selectively binds to members of Ena/VASP protein
FT               family"
XX
PN   WO200031252-A1.
XX
PD   02-JUN-2000.
XX
PF   26-NOV-1999;  99WO-EP009215.
XX
PR   26-NOV-1998;  98EP-00122441.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Behl C,  Klostermann A;
XX
DR   WPI; 2000-400065/34.
DR   P-PSDB; AAY71460.
XX
PT   Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT   therapeutic agent, for modulating immune system, in gene therapy or for
PT   effecting differentiation, cytoskeletal stabilization and/or plasticity.
XX
PS   Claim 1; Fig 2; 53pp; English.
XX
CC   The present sequence is a cDNA encoding transmembranous human semaphorin
CC   6A-1 ((HSA)SEMA6A-1) which is involved in neuronal development and
CC   regeneration mechanisms during apoptosis. Semaphorin is a family of
CC   proteins displaying secreted or transmembrane-based repulsive guidance
CC   cues critically involved in neuronal development. The present sequence
CC   was isolated from human 1-ZAP Express cDNA library which was screened
CC   using a PCR fragment amplified from human neuroblastoma cell line SK-N-MC
CC   cDNA. The (HSA)SEMA6A-1 protein contains a Zyxin-like domain that
CC   selectively binds to members of Ena/VASP protein family especially Evl.
CC   Expression of (HSA)SEMA6A-1 is highest in embryonic brain and kidney and
CC   moderate in lung. The present sequence is useful as diagnostic and
CC   therapeutic agents, for modulating the immune system, in gene therapy,
CC   for effecting differentiation, cytoskeletal stabilisation and plasticity
XX
SQ   Sequence 3862 BP; 971 A; 1111 C; 967 G; 813 T; 0 U; 0 Other;

Query Match          100.0%;  Score 3093;  DB 3;  Length 3862;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 3093;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60

```

Db	658	 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC	717
Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	120
Db	718	 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	777
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	778	 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	837
Qy	181	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	838	 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	897
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	898	 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	957
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT	360
Db	958	 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT	1017
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	1018	 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	1077
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	1078	 AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	1137
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	1138	 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	1197
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	1198	 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	1257
Qy	601	CTTGGAGAAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660
Db	1258	 CTTGGAGAAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	1317
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGAAAATAGCA	720
Db	1318	 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGAAAATAGCA	1377
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	1378	 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	1437
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	840
Db	1438	 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	1497
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900

Db	1498	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	1557
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1558	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1617
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1618	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1677
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1678	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1737
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1738	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1797
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1798	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1857
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1858	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTTCCTGAGAACAATGGTCAGATACCGCCTT	1917
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1918	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1977
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1978	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	2037
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT	1440
Db	2038	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT	2097
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	2098	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	2157
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	2158	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	2217
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	2218	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	2277
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	2278	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	2337
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	2338	AATACAGATGGTCTGGGGGACTGTCACAATTCTTTGTGGCACTGAATGGGCATTCCAGT	2397

Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	2398	TCCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	2457
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2458	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2517
Qy	1861	GCAGTGTCTTCCCATTAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAA	1920
Db	2518	GCAGTGTCTTCCCATTAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAA	2577
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCTGGCTTTCGTC	1980
Db	2578	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCTGGCTTTCGTC	2637
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2638	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2697
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2698	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2757
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2758	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2817
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2818	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2877
Qy	2221	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2878	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2937
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2938	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2997
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2998	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	3057
Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	2460
Db	3058	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	3117
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2520
Db	3118	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	3177
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	3178	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	3237

Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC	2640
Db	3238	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC	3297
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	3298	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	3357
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	3358	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	3417
Qy	2761	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAAC	2820
Db	3418	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAAC	3477
Qy	2821	TCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2880
Db	3478	TCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	3537
Qy	2881	CCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	2940
Db	3538	CCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	3597
Qy	2941	GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG	3000
Db	3598	GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG	3657
Qy	3001	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCTTTCC	3060
Db	3658	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCTTTCC	3717
Qy	3061	ACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3718	ACATCCATGAAGCCCAATGATGCGTGTACATAA	3750

RESULT 2

AAA93617

ID AAA93617 standard; DNA; 3498 BP.

XX

AC AAA93617;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
 KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.

XX
 OS Homo sapiens.
 XX
 PN WO200053742-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US006280.
 XX
 PR 09-MAR-1999; 99US-0123667P.
 PR 08-MAR-2000; 2000US-0520781P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA;
 XX
 DR WPI; 2000-594318/56.
 DR P-PSDB; AAB23030.
 XX
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders.
 XX
 PS Claim 3; Fig 2; 151pp; English.
 XX
 CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
 CC the invention are either secreted or membrane-associated proteins and act
 CC as regulator of cellular proliferation and differentiation. SECX proteins
 CC or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC proteins and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of a
 CC SECX protein with other cellular proteins may be useful to modulate the
 CC activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in a
 CC biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
 CC or traumatic wounds, spinal cord injury), and skeletal disorders
 XX
 SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

 Query Match 98.2%; Score 3038; DB 3; Length 3498;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

Qy	1	ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC	60
Db	214	ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC	273
Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	120
Db	274	CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	333
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	334	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	393
Qy	181	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	394	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	453
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	454	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	513
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	360
Db	514	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	573
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	574	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	633
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	634	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	693
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	694	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	753
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	754	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	813
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660
Db	814	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	873
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	874	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	933
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	934	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	993
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGCGCGC	840
Db	994	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGCGCGC	1053

Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTC AACATTCTCCAGGCAGTTACA	900
Db	1054	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTC AACATTCTCCAGGCAGTTACA	1113
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1114	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1173
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCATGACATGCTTGACATTGCCAGTGTTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1413
Qy	1201	GCAGTGGCCTCCATCTTCAACAGGCCATGGTTCTTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	GCAGTGGCCTCCATCTTCAACAGGCCATGGTTCTTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTTCTA	1593
Qy	1381	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740

Db	1894	 AATACAGATGGTCTGGGGGACTGTCACAATTCTTTGTGGCACTGAATGGGCATTCCAGT	1953
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1954	 TCCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	2013
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2014	 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2073
Qy	1861	GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAA	1920
Db	2074	 GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAA	2133
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2134	 GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	2193
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2194	 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2253
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2254	 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2313
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2314	 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2373
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2374	 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2433
Qy	2221	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2280
Db	2434	 ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2493
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2494	 ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2553
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2554	 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2613
Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATC	2460
Db	2614	 ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATC	2673
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCCAG	2520
Db	2674	 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCCAG	2733
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580

Db	2734	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2793
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC	2640
Db	2794	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC	2853
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2854	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2913
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2914	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2973
Qy	2761	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAGAAACAACACTAA	2819
Db	2974	CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	3033
Qy	2820	CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC	2878
Db	3034	CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC	3093
Qy	2879	CGCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2938
Db	3094	CGCCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	3153
Qy	2939	CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	2998
Db	3154	CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	3213
Qy	2999	TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT	3058
Db	3214	TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT	3273
Qy	3059	CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3274	CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3308

RESULT 3

ADA23280

ID ADA23280 standard; cDNA; 3498 BP.

XX

AC ADA23280;

XX

DT 20-NOV-2003 (first entry)

XX

DE cDNA encoding human SECX polypeptide, SEC2.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
 KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
 KW antiallergic; cardiant; dermatological; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003054514-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 19-SEP-2001; 2001US-00957187.
 XX
 PR 09-MAR-1999; 99US-0123667P.
 PR 04-JAN-2000; 2000US-0174485P.
 PR 08-MAR-2000; 2000US-00520781.
 PR 19-SEP-2000; 2000US-0233798P.
 PR 20-SEP-2000; 2000US-0234082P.
 XX
 PA (SHIM/) SHIMKETS R A.
 PA (LARO/) LAROCHELLE W J.
 XX
 PI Shimkets RA, Larochelle WJ;
 XX
 DR WPI; 2003-540616/51.
 DR P-PSDB; ADA23281.
 XX
 PT New SECX nucleic acids, useful for treating or diagnosing a disorder
 PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
 PT and autoimmune disease.
 XX
 PS Claim 3; Fig 2; 118pp; English.
 XX
 CC The present invention relates to the isolation of human secreted or
 CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
 CC polynucleotide sequences encoding them. Also disclosed is a method for
 CC screening for a modulator of activity or latency of SECX. The SECX
 CC polypeptide and polynucleotide sequences may be used for treating or
 CC preventing SECX-associated disorders such as lung cancer, cardiovascular
 CC and oncology diseases, immune disorders, autoimmune diseases, transplant
 CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
 CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
 CC cord injuries, and skeletal disorders. The present sequence encodes a
 CC SECX polypeptide of the invention.
 XX
 SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

Db 274 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy 121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
 |||

Db 334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy 181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
 |||

Db 394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy 241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
 |||

Db 454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 513

Qy 301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAACATAAGGATGAGTGCCACAACCTTT 360
 |||

Db 514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAACATAAGGATGAGTGCCACAACCTTT 573

Qy 361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTGTCTGTGGAACATAATGCCTTC 420
 |||

Db 574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTGTCTGTGGAACATAATGCCTTC 633

Qy 421 AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
 |||

Db 634 AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy 481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
 |||

Db 694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy 541 AAACATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
 |||

Db 754 AAACATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy 601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA 660
 |||

Db 814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA 873

Qy 661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
 |||

Db 874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy 721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
 |||

Db 934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy 781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC 840
 |||

Db 994 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC 1053

Qy 841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA 900
 |||

Db 1054 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA 1113

Qy 901 GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
 |||

Db 1114 GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1173

Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	TCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACCCGCTCATGGATGAG	1413
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1593
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGTGTT	1620
Db	1774	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGTGTT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1953
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1954	TCCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	2013

Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2014	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2073
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAAA	1920
Db	2074	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAAA	2133
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2134	GGCCACGACCAGCTGGTTCCCGTCACCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	2193
Qy	1981	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2194	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2253
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2254	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2313
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2314	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2373
Qy	2161	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2374	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2433
Qy	2221	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2434	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2493
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2494	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2553
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2554	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2613
Qy	2401	ACGGACCTGCCCCGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2460
Db	2614	ACGGACCTGCCCCGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2673
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2520
Db	2674	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2733
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2734	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2793
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2794	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2853
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700

Db	2854	 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2913
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2914	 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2973
Qy	2761	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA	2819
Db	2974	 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	3033
Qy	2820	CTCCTCCAATTCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC	2878
Db	3034	 CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC	3093
Qy	2879	CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2938
Db	3094	 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	3153
Qy	2939	CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGC	2998
Db	3154	 CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGC	3213
Qy	2999	TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT	3058
Db	3214	 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT	3273
Qy	3059	CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3274	 CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3308

RESULT 4

ABX71103

ID ABX71103 standard; cDNA; 4280 BP.

XX

AC ABX71103;

XX

DT 05-MAR-2003 (first entry)

XX

DE Novel human cDNA sequence #328.

XX

KW Human; gene; ss; nervous system disorder; peripheral neuropathy;
KW Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
KW neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;
KW ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
KW fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
KW coagulation disorder; cancer; tumour; inflammatory disease; septic shock;
KW Crohn's disease; anaphylaxis; proliferation; chemotactic;
KW differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
KW haemostatic; antiinflammatory; expressed sequence tag; EST.

XX

OS Homo sapiens.

XX

PN WO200281731-A2.

XX
 PD 17-OCT-2002.
 XX
 PF 29-JAN-2002; 2002WO-US001222.
 XX
 PR 30-JAN-2001; 2001US-00774528.
 XX
 PA (HYSE-) HYSEQ INC.
 PA (GOOD/) GOODRICH R W.
 XX
 PI Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 DR WPI; 2003-058563/05.
 XX
 PT Novel polypeptide useful for treating neurodegenerative diseases, myeloid
 PT or lymphoid cell disorders, bone disorders, mechanical and traumatic
 PT disorders, coagulation disorders, and inflammatory diseases.
 XX
 PS Claim 1; Page; 612pp; English.
 XX
 CC This invention relates to the cDNA sequences encoding an isolated novel
 CC human polypeptide. The protein encoded by the nucleic acid of the
 CC invention is useful for treating central and peripheral nervous system
 CC diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic
 CC lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease,
 CC Alzheimer's disease); autoimmune disease (e.g. systemic lupus
 CC erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus)
 CC ; myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia)
 CC ; wounds, ulcers, burns; bone disorders (e.g. osteoporosis,
 CC osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head
 CC trauma); lung or liver fibrosis; reperfusion injury in various tissues;
 CC bacterial, viral or fungal infections; allergic conditions such as
 CC allergic rhinitis, asthma; coagulation disorders (e.g. haemophilia);
 CC cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's
 CC disease, anaphylaxis). The protein may be used to inhibit the growth,
 CC infection or function of infectious agents such as bacteria, fungi,
 CC viruses, or to effect bodily characteristics, biorhythms or circadian
 CC cycles of rhythms. The protein may also have
 CC proliferation/differentiation, stem cell growth factor, haematopoiesis
 CC regulation, immune stimulating or suppressing, chemotactic/chemokinetic,
 CC haemostatic and thrombolytic, receptor/ligand, and antiinflammatory
 CC activities. The cDNA sequences of the invention are useful for expressing
 CC recombinant protein for analysis. The present sequence represents a novel
 CC human cDNA sequence of the invention, this sequence is an expressed
 CC sequence tag (EST) and was identified using subtractive hybridisation
 XX
 SQ Sequence 4280 BP; 1185 A; 1165 C; 1001 G; 929 T; 0 U; 0 Other;

Query Match 98.0%; Score 3032; DB 7; Length 4280;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

Qy 1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
 |||
 Db 267 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 326

Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	120
Db	327	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	386
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	387	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	446
Qy	181	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	447	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	506
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	507	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	566
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT	360
Db	567	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT	626
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	627	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	686
Qy	421	AACCCCTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	687	AACCCCTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	746
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	747	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	806
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	807	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	866
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	867	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	926
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAATAGCA	720
Db	927	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAATAGCA	986
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAAT	780
Db	987	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAAT	1046
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	840
Db	1047	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	1106
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1107	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1166
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960

Db	1167	 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1226
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1227	 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1286
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1287	 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1346
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1347	 GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1406
Qy	1141	TCCAATGAGTTCCTTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1407	 TCCAATGAGTTCCTTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1466
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1467	 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1526
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1527	 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1586
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1587	 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1646
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1647	 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1706
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1707	 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1766
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1767	 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1826
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1827	 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1886
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1887	 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1946
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1947	 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	2006
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749

Db	2007	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	2066
Qy	1750	CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	2067	CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2126
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	2127	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	2186
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2187	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	2246
Qy	1930	CAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	2247	CAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2306
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2307	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2366
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2367	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2426
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2427	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2486
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2487	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2546
Qy	2230	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289
Db	2547	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2606
Qy	2290	CTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2607	CTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2666
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2409
Db	2667	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2726
Qy	2410	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2469
Db	2727	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2786
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2529
Db	2787	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2846
Qy	2530	GAGGACCAGGCCGCCCACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2847	GAGGACCAGGCCGCCCACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2906

Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	2907	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2966
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	2967	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	3026
Qy	2710	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769
Db	3027	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	3086
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	2829
Db	3087	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	3146
Qy	2830	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCG	2889
Db	3147	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCG	3206
Qy	2890	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	2949
Db	3207	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	3266
Qy	2950	TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3009
Db	3267	TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3326
Qy	3010	CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG	3069
Db	3327	CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG	3386
Qy	3070	AAGCCCAATGATGCGTGTACATAA	3093
Db	3387	AAGCCCAATGATGCGTGTACATAA	3410

RESULT 5

ADA23361

ID ADA23361 standard; cDNA; 4250 BP.

XX

AC ADA23361;

XX

DT 20-NOV-2003 (first entry)

XX

DE cDNA encoding human SECX polypeptide, SEC15.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;

KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;

KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;

KW cardiovascular disease; oncology disease; immune disorder;

KW autoimmune disease; transplant rejection; allergy; AIDS; infections;

KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;

KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;

KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelle WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23362.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Page 13-14; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.
XX
SQ Sequence 4250 BP; 1168 A; 1161 C; 995 G; 926 T; 0 U; 0 Other;

Query Match 97.8%; Score 3025.6; DB 8; Length 4250;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3089; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

```
Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
          |||
Db      250 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTGCGCATGGCAACTATACAAAACAGTATCCGGTG 120
          |||
Db      310 CCAGAAGATTCTGAGCCAATCAGTATTTGCGCATGCAACTATACAAAACAGTATCCGGTG 369
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Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	370	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	429
Qy	181	ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	430	ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	489
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	490	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	549
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT	360
Db	550	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT	609
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC	420
Db	610	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC	669
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	670	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	729
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	730	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	789
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	790	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	849
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	850	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	909
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	910	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	969
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	970	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	1029
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	1030	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	1089
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	900
Db	1090	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	1149
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTCTACACCTTATAAC	960
Db	1150	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTCTACACCTTATAAC	1209

Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1210	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1269
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1270	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1329
Qy	1081	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1330	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1389
Qy	1141	TCCAATGAGTTCCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1390	TCCAATGAGTTCCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1449
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1450	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1509
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1510	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1569
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1570	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1629
Qy	1381	AATGACAGCCTTTTCTGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1630	AATGACAGCCTTTTCTGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1689
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1690	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1749
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1750	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1809
Qy	1561	TGTAACAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1810	TGTAACAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1869
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1870	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1929
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1930	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1989
Qy	1727	-----ATGGGCATTCCAGTTCCCTCTTG	1749
Db	1990	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCCTCTTG	2049
Qy	1750	CCCAGCACACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809

Db	2050	 CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2109
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	2110	 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	2169
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2170	 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	2229
Qy	1930	CAGCTGGTTCCCGTCACCCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	2230	 CAGCTGGTTCCCGTCACCCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2289
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2290	 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2349
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2350	 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2409
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2410	 AAGCTCAGCGGCCTCTTTGGGGACACTCATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2469
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2470	 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2529
Qy	2230	AAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289
Db	2530	 AAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2589
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2590	 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2649
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2409
Db	2650	 ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2709
Qy	2410	CCCCTGCGGGCCTCCCCCAGCCACATCCCAGCGTGGTGGTCTGCCCATCACGCAGCAG	2469
Db	2710	 CCCCTGCGGGCCTCCCCCAGCCACATCCCAGCGTGGTGGTCTGCCCATCACGCAGCAG	2769
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2529
Db	2770	 GGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2829
Qy	2530	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2830	 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2889
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649

Db	2890	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2949
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	2950	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	3009
Qy	2710	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769
Db	3010	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	3069
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	2829
Db	3070	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	3129
Qy	2830	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCG	2889
Db	3130	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCG	3189
Qy	2890	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	2949
Db	3190	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	3249
Qy	2950	TCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGCTGAAGCGTACG	3009
Db	3250	TCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGCTGAAGCGTACG	3309
Qy	3010	CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTCCACATCCATG	3069
Db	3310	CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTCCACATCCATG	3369
Qy	3070	AAGCCCAATGATGCGTGTACATAA	3093
Db	3370	AAGCCCAATGATGCGTGTACATAA	3393

RESULT 6

AAH18729

ID AAH18729 standard; cDNA; 6060 BP.

XX

AC AAH18729;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:19004.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

Db	121	TAGGGACCATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAG	180
Qy	276	CAAAAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA	335
Db	181	CAAAAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA	240
Qy	336	ACATAAGGATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATT	395
Db	241	ACATAAGGATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATT	300
Qy	396	GTTTGTCTGTGGAACATAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATT	455
Db	301	GTTTGTCTGTGGAACATAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATT	360
Qy	456	GGAACCATTCGGGGATGAATTTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC	515
Db	361	GGAACCATTCGGGGATGAATTTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC	420
Qy	516	CAACGTTGCACTGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGC	575
Db	421	CAACGTTGCACTGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGC	480
Qy	576	CATTGACGCAGTCATTTACCGGAGTCTTGAGAAAGCCCTACCCTGCGGACCGTCAAGCA	635
Db	481	CATTGACGCAGTCATTTACCGGAGTCTTGAGAAAGCCCTACCCTGCGGACCGTCAAGCA	540
Qy	636	CGATTCAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT	695
Db	541	CGATTCAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT	600
Qy	696	CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC	755
Db	601	CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC	660
Qy	756	AAGAGTGGCTCAGGTTTGTAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA	815
Db	661	AAGAGTGGCTCAGGTTTGTAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA	720
Qy	816	GTGGACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTTA	875
Db	721	GTGGACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTTA	780
Qy	876	TTTCAACATTCTCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCT	935
Db	781	TTTCAACATTCTCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCT	840
Qy	936	GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT	995
Db	841	GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT	900
Qy	996	GCTTGACATTGCCAGTGTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC	1055
Db	901	GCTTGACATTGCCAGTGTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC	960
Qy	1056	CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC	1115
Db	961	CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC	1020

Qy	1116	ATCCTCCTTAGAAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCAT	1175
Db	1021	ATCCTCCTTAGAAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCAT	1080
Qy	1176	CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT	1235
Db	1081	CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT	1140
Qy	1236	GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA	1295
Db	1141	GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA	1200
Qy	1296	TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC	1355
Db	1201	TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC	1260
Qy	1356	CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA	1415
Db	1261	CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA	1320
Qy	1416	CAACTCTG-AAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC	1474
Db	1321	CAACTCTGAAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC	1380
Qy	1475	TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC	1534
Db	1381	TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC	1440
Qy	1535	TTGGCCGGTGTGAACGACATGGGAAGTGT-AAAAAACCTGTATTGCCTCCAGAGACCCA	1593
Db	1441	TTGGCCGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCA	1500
Qy	1594	TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG	1653
Db	1501	TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG	1560
Qy	1654	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1713
Db	1561	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1620
Qy	1714	TTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCCAGCACCAACCACATCAGATTCTG	1773
Db	1621	TTTGTGGCACTGAATGGGCATTCTAGTTCCTCTTGCCCAGCACCAACCACATCAGATTCTG	1680
Qy	1774	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1833
Db	1681	ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC	1740
Qy	1834	TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	1893
Db	1741	TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG	1800
Qy	1894	GGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG	1953
Db	1801	GGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG	1860

Qy	1954	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	2013
Db	1861	GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC	1920
Qy	2014	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	2073
Db	1921	TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC	1980
Qy	2074	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC	2133
Db	1981	ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC	2040
Qy	2134	ACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2193
Db	2041	ACTCAATCCGAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG	2100
Qy	2194	CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGAC	2253
Db	2101	CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACTAGCACCTGGAC	2160
Qy	2254	CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC	2313
Db	2161	CTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC	2220
Qy	2314	CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG	2373
Db	2221	CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG	2280
Qy	2374	CCCCCATGGGGCTCCCTGTGATTCCACGGACCTGCCCCTGCGGGCCTCCCCAGCCAC	2433
Db	2281	CCCCCATGGGGCTCCCTGTGATTCCACGGACCTGCCCCTGCGGGCCTCCCCAGCCAC	2340
Qy	2434	ATCCCCAGCGTGGTGGTCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC	2493
Db	2341	ATCCCCAGCGTGGTGGTCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC	2400
Qy	2494	CAGCCCCAAAATGAGCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG	2553
Db	2401	CAGCCCCAAAATGAGCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG	2460
Qy	2554	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2613
Db	2461	TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG	2520
Qy	2614	GAGAACCTGGACAGCCTGCCCCCAAAGTTCACAGCGGGAGGCCTCCCTGGGTCCCCCG	2673
Db	2521	GAGAACCTGGACAGCCTGCCCCCAAAGTTCACAGCGGGAGGCCTCCCTGGGTCCCCCG	2580
Qy	2674	GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC	2733
Db	2581	GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC	2640
Qy	2734	TACGGGGTTGACTATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGCC	2793
Db	2641	TACGGGGTTGACTATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGCC	2700
Qy	2794	ACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG	2853

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Db      2701 ACCACTCTCAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG 2760
Qy      2854 AGCTTTGGCAGGGGAGACAACCCGCCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGTG 2913
Db      2761 AGCTTTGGCAGGGGAGACAACCCGCCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGTG 2820
Qy      2914 CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCC 2973
Db      2821 CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCC 2880
Qy      2974 TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC 3033
Db      2881 TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC 2940
Qy      3034 CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
Db      2941 CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATAA 3000

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RESULT 7

AAV44295

ID AAV44295 standard; cDNA; 3550 BP.

XX

AC AAV44295;

XX

DT 06-OCT-1998 (first entry)

XX

DE Human secreted protein clone CJ145_1 cDNA.

XX

KW Secreted protein; human fetal brain; nutrition; cytokine; stimulant;
KW cell proliferation; differentiation; immune system; suppressor; ligand;
KW regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW anti-inflammatory; ds.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	126..3053
FT		/*tag= a
FT		/product= "secreted protein"
FT		/note= "isolated from clone CJ145_1"

XX

PN WO9827205-A2.

XX

PD 25-JUN-1998.

XX

PF 17-DEC-1997; 97WO-US023330.

XX

PR 18-DEC-1996; 96US-00769192.

PR 13-JAN-1997; 97US-00783401.

PR 16-DEC-1997; 97US-00991872.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;

PI Spaulding V, Agostino MJ;
 XX
 DR WPI; 1998-362774/31.
 DR P-PSDB; AAW64221.
 XX
 PT New polynucleotides and secreted proteins - obtained from human foetal
 PT brain, human adult testes, human adult brain and human adult salivary
 PT gland cDNA libraries.
 XX
 PS Claim 17a; Page 69-71; 110pp; English.
 XX
 CC This sequence encodes a novel secreted protein from clone CJ145_1
 CC isolated from a human fetal brain cDNA library. This protein has
 CC applications for nutritional use, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating or suppressing
 CC activity, hematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombotic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
 CC activity and other activities
 XX
 SQ Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 0 U; 1 Other;

Query Match 88.8%; Score 2746.2; DB 2; Length 3550;
 Best Local Similarity 94.5%; Pred. No. 0;
 Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;

Qy	1	ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC	60
Db	126	ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC	185
Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	120
Db	186	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	245
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	246	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	305
Qy	181	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	306	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	365
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA	300
		:	
Db	366	ATAGACACATCACACACSGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA	425
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT	360
Db	426	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT	485
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	486	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	545
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480

Db	546	AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTGAGC	605
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	606	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	665
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	666	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	725
Qy	601	CTTGGAGAAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660
Db	726	CTTGGAGAAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	785
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTCAGGGAAATAGCA	720
Db	786	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTCAGGGAAATAGCA	845
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAT	780
Db	846	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAT	905
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	840
Db	906	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	965
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	966	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1025
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1026	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1085
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1086	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1145
Qy	1021	GGGAGATTCAAGGAACAGAACTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1146	GGGAGATTCAAGGAACAGAACTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1205
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1206	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1265
Qy	1141	TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1266	TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1325
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCTTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1326	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCTTGAGAACAATGGTCAGATACCGCCTT	1385
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1386	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1445

Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1446	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1505
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1506	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1565
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1566	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1625
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1626	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1685
Qy	1561	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1686	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1745
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1746	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1805
Qy	1681	AATACAGATGGTCTGGGGGACTGTACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1806	AATACAGATGGTCTGGGGGACTGTACAATTCCTTTGTGGCACTGAAT-----	1853
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1854	-----	1853
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	1854	-----	1853
Qy	1861	GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA	1920
Db	1854	-----GGAGTGATTCGGGAAAGTTACCTCAAA	1880
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	1881	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1940
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	1941	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2000
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2001	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2060
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2061	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2120

Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2121	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2180
Qy	2221	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2181	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2240
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2241	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2300
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2301	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2360
Qy	2401	ACGGACCTGCCCCTGCGGGCTCCCCAGCCACATCCCAGCGTGGTGGTCTGCCCATC	2460
Db	2361	ACGGACCTGCCCCTGCGGGCTCCCCAGCCACATCCCAGCGTGGTGGTCTGCCCATC	2420
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2520
Db	2421	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2480
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2481	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATTTTCAGC	2540
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2541	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2600
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2601	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTTTCAGACCGGTTTA	2660
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2661	AGCAAGCGGCTGGAAATGCACCACTCCTTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2720
Qy	2761	CCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAAC	2820
Db	2721	CCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAAC	2780
Qy	2821	TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2880
Db	2781	TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2840
Qy	2881	CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGCCAGGCC	2940
Db	2841	CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGCCAGGCC	2900
Qy	2941	GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTGCGGGCTG	3000
Db	2901	GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTGCGGGCTG	2960
Qy	3001	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCC	3060


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Db      2961 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCCTTCC 3020

Qy      3061 ACATCCATGAAGCCCAATGATGCGGTGTACATAA 3093
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Db      3021 ACATCCATGAAGCCCAATGATGCGGTGTACATAA 3053

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RESULT 8

AAF98469

ID AAF98469 standard; cDNA; 3550 BP.

XX

AC AAF98469;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human cDNA clone CJ145_1 sequence SEQ ID 160.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.

XX

PD 22-MAR-2001.

XX

PF 14-SEP-2000; 2000WO-US025135.

XX

PR 17-SEP-1999; 99US-00398829.

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PA (GEMY) GENETICS INST INC.

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PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

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DR WPI; 2001-244801/25.

DR P-PSDB; AAB90731.

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PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
 PT cytokine and cell proliferation/differentiation activity, the immune
 PT system and hematopoiesis regulating activity.

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PS Disclosure; Page 486-487; 557pp; English.

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CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;

CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
CC activity. Included in the invention are probes represented in AAF98490 -
CC AAF98572 which are specific for the cDNA clones encoding the secreted
CC proteins

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SQ Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 0 U; 1 Other;

Query Match 88.8%; Score 2746.2; DB 5; Length 3550;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC 60
          |||
Db     126 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC 185

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTGCGCATGGCAACTATACAAAACAGTATCCGGTG 120
          |||
Db     186 CCAGAAGATTCTGAGCCAATCAGTATTTGCGCATGGCAACTATACAAAACAGTATCCGGTG 245

Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
          |||
Db     246 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 305

Qy     181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
          |||
Db     306 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 365

Qy     241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
          |||:|||
Db     366 ATAGACACATCACACACSGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 425

Qy     301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 360
          |||
Db     426 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 485

Qy     361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
          |||
Db     486 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 545

Qy     421 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
          |||
Db     546 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 605

Qy     481 GGAATGGCCAGATGCCCATATGATGCCAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
          |||
Db     606 GGAATGGCCAGATGCCCATATGATGCCAACATGCCAACGTTGCACTGTTTGCAGATGGA 665

Qy     541 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
          |||
Db     666 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 725

Qy     601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
          |||
Db     726 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 785

Qy     661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Db	786	 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	845
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	846	 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	905
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	840
Db	906	 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	965
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	966	 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1025
Qy	901	GATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1026	 GATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1085
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1086	 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1145
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1146	 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1205
Qy	1081	GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1206	 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1265
Qy	1141	TCCAATGAGTTCCTTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1266	 TCCAATGAGTTCCTTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1325
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1326	 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1385
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1386	 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1445
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1446	 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1505
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1506	 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1565
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1566	 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1625
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560

Db	1626	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1685
Qy	1561	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1686	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1745
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1746	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1805
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1806	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT----- ₀ -----	1853
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1854	-----	1853
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	1854	-----	1853
Qy	1861	GCAGTGTCTTCCCATATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAAA	1920
Db	1854	-----GGAGTGATTGCGGAAAGTTACCTCAAA	1880
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCTGGCTTTTCGTC	1980
Db	1881	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCTGGCTTTTCGTC	1940
Qy	1981	ATGGGGGCGCTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	1941	ATGGGGGCGCTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2000
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2001	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2060
Qy	2101	AGCGTCACCAAGCTCAGCGGCCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2061	AGCGTCACCAAGCTCAGCGGCCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2120
Qy	2161	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2121	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2180
Qy	2221	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2280
Db	2181	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2240
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2241	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2300
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2301	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2360

Qy	2401	ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	2460
Db	2361	ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	2420
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2520
Db	2421	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2480
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2481	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATTTTCAGC	2540
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC AAA	2640
Db	2541	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC AAA	2600
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2601	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTTTCAGACCGGTTTA	2660
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2661	AGCAAGCGGCTGGAAATGCACCACTCCTTTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2720
Qy	2761	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC	2820
Db	2721	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC	2780
Qy	2821	TCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2880
Db	2781	TCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG	2840
Qy	2881	CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	2940
Db	2841	CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC	2900
Qy	2941	GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG	3000
Db	2901	GTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTG	2960
Qy	3001	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC	3060
Db	2961	AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC	3020
Qy	3061	ACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3021	ACATCCATGAAGCCCAATGATGCGTGTACATAA	3053

RESULT 9

AAA93618

ID AAA93618 standard; DNA; 3333 BP.

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AC AAA93618;

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DT 16-JAN-2001 (first entry)

XX
 DE Human semaphorin protein-like splice variant SECX 2864933-2 DNA.
 XX
 KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
 KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200053742-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US006280.
 XX
 PR 09-MAR-1999; 99US-0123667P.
 PR 08-MAR-2000; 2000US-0520781P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA;
 XX
 DR WPI; 2000-594318/56.
 DR P-PSDB; AAB23031.
 XX
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and
 PT neurological disorders.
 XX
 PS Claim 3; Fig 3; 151pp; English.
 XX
 CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
 CC the invention are either secreted or membrane-associated proteins and act
 CC as regulator of cellular proliferation and differentiation. SECX proteins
 CC or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC proteins and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of a
 CC SECX protein with other cellular proteins may be useful to modulate the
 CC activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used to detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in a
 CC biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or

CC prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders

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SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 0 U; 1 Other;

Query Match 87.2%; Score 2698; DB 3; Length 3333;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;

```
Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
          |||
Db    214 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy     61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
          |||
Db    274 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy    121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
          |||
Db    334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy    181 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
          |||
Db    394 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy    241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
          |||
Db    454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 513

Qy    301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 360
          |||
Db    514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 573

Qy    361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
          |||
Db    574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 633

Qy    421 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
          |||
Db    634 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy    481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
          |||
Db    694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy    541 AAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
          |||
Db    754 AAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy    601 CTTGGAGAAAGCCCTACCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA 660
          |||
Db    814 CTTGGAGAAAGCCCTACCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA 873
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Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	874	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	933
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	780
Db	934	GTGGAGTATAACACCATGGGAAAGGTAGTTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	993
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGC	840
Db	994	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGC	1053
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1054	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1113
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGCGCAACGTTTTCTACACCTTATAAC	960
Db	1114	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGCGCAACGTTTTCTACACCTTATAAC	1173
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTCTTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	GTTCTTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1413
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1593
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713

Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT-----	1941
Qy	1741	TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1942	-----	1941
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	1942	-----	1941
Qy	1861	GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAA	1920
Db	1942	-----GGAGTGATTCGGGAAAGTTACCTCAA	1968
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	1969	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	2028
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2029	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2088
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2089	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTACCCACTCGCGCCGGGGCTCCATGAGC	2148
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2149	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2208
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2209	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2268
Qy	2221	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2269	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2328
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2329	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2388
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400

Db	2389	 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2448
Qy	2401	ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATC	2460
Db	2449	 ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATC	2508
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCAG	2520
Db	2509	 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCAG	2568
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCCACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2569	 ATGGCGCTGGAGGACCAGGCCGCCCACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2628
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2629	 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2688
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2689	 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2748
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2749	 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2808
Qy	2761	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAGAAACAACACTAA	2819
Db	2809	 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	2868
Qy	2820	CTCCTCCAATTCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC	2878
Db	2869	 CCCCGACAATTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC	2928
Qy	2879	CGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2938
Db	2929	 CGCCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2988
Qy	2939	CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTTCGGGGC	2998
Db	2989	 CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTTCGGGGC	3048
Qy	2999	TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTT	3058
Db	3049	 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTT	3108
Qy	3059	CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3109	 CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3143

RESULT 10

ADA23282

ID ADA23282 standard; cDNA; 3333 BP.

XX

AC ADA23282;

XX
 DT 20-NOV-2003 (first entry)
 XX
 DE cDNA encoding human SECX polypeptide, SEC3 #1.
 XX
 KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
 KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
 KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
 KW cardiovascular disease; oncology disease; immune disorder;
 KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
 KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
 KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
 KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
 KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
 KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
 KW antiallergic; cardiant; dermatological; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003054514-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 19-SEP-2001; 2001US-00957187.
 XX
 PR 09-MAR-1999; 99US-0123667P.
 PR 04-JAN-2000; 2000US-0174485P.
 PR 08-MAR-2000; 2000US-00520781.
 PR 19-SEP-2000; 2000US-0233798P.
 PR 20-SEP-2000; 2000US-0234082P.
 XX
 PA (SHIM/) SHIMKETS R A.
 PA (LARO/) LAROCHELLE W J.
 XX
 PI Shimkets RA, Larochelle WJ;
 XX
 DR WPI; 2003-540616/51.
 DR P-PSDB; ADA23283.
 XX
 PT New SECX nucleic acids, useful for treating or diagnosing a disorder
 PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
 PT and autoimmune disease.
 XX
 PS Claim 3; Fig 3; 118pp; English.
 XX
 CC The present invention relates to the isolation of human secreted or
 CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
 CC polynucleotide sequences encoding them. Also disclosed is a method for
 CC screening for a modulator of activity or latency of SECX. The SECX
 CC polypeptide and polynucleotide sequences may be used for treating or
 CC preventing SECX-associated disorders such as lung cancer, cardiovascular
 CC and oncology diseases, immune disorders, autoimmune diseases, transplant
 CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
 CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
 CC cord injuries, and skeletal disorders. The present sequence encodes a
 CC SECX polypeptide of the invention.

XX

SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 0 U; 1 Other;

Query Match 87.2%; Score 2698; DB 8; Length 3333;

Best Local Similarity 93.9%; Pred. No. 0;

Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;

```
Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
      |||
Db     214 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
      |||
Db     274 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
      |||
Db     334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy     181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
      |||
Db     394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy     241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
      |||
Db     454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 513

Qy     301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 360
      |||
Db     514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 573

Qy     361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 420
      |||
Db     574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 633

Qy     421 AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
      |||
Db     634 AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy     481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
      |||
Db     694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy     541 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
      |||
Db     754 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy     601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
      |||
Db     814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873

Qy     661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
      |||
Db     874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy     721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
      |||
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Db	934	GTGGAGTATAACACCATGGGAAAGGTAGTTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	993
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	994	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	1053
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1054	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1113
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1114	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1173
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1413
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1593
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGCCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGCCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833

Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT-----	1941
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1942	-----	1941
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	1942	-----	1941
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAA	1920
Db	1942	-----GGAGTGATTCGGGAAAGTTACCTCAA	1968
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	1969	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	2028
Qy	1981	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2029	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2088
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2089	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2148
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2149	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2208
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2209	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2268
Qy	2221	ATGCTCATTAAGCAGACCAGCACACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2269	ATGCTCATTAAGCAGACCAGCACACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2328
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2329	ACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCACCCGCGAGTGGGAGAGGAAC	2388
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCTGTGATTCCC	2400
Db	2389	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCTGTGATTCCC	2448
Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2460
Db	2449	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2508

Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2520
Db	2509	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2568
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2569	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2628
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2629	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2688
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2689	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2748
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2749	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTAC	2808
Qy	2761	CCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAGAAACAACACTAA	2819
Db	2809	CCCACGAACCTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	2868
Qy	2820	CTCCTCCAATTCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC	2878
Db	2869	CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC	2928
Qy	2879	CGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2938
Db	2929	CGCCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2988
Qy	2939	CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	2998
Db	2989	CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	3048
Qy	2999	TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTT	3058
Db	3049	TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTT	3108
Qy	3059	CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3109	CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3143

RESULT 11

AAS68807

ID AAS68807 standard; cDNA; 3039 BP.

XX

AC AAS68807;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #4611.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

```
XX Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG04620.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 4611; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 U; 0 Other;

Query Match          71.8%; Score 2221.8; DB 5; Length 3039;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2408; Conservative 0; Mismatches 167; Indels 66; Gaps 2;

Qy      519 CGTTGCACTGTTTGCAGATGGAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCAT 578
        | | | ||| | ||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db      399 CCTGACTCTGTCTCCAGATGGAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCAT 458
```


Qy	579	TGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGA	638
Db	459	TGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGA	518
Qy	639	TTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTA	698
Db	519	TTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTA	578
Qy	699	CTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAG	758
Db	579	CTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAG	638
Qy	759	AGTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTG	818
Db	639	AGTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTG	698
Qy	819	GACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTT	878
Db	699	GACGTCGTTCCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTT	758
Qy	879	CAACATTCTCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGC	938
Db	759	CAACATTCTCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGC	818
Qy	939	AACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCT	998
Db	819	AACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCT	878
Qy	999	TGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTG	1058
Db	879	TGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTG	938
Qy	1059	GACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATC	1118
Db	939	GACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATC	998
Qy	1119	CTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACCTCATCAA	1178
Db	999	CTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACCTCATCAA	1058
Qy	1179	GACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAG	1238
Db	1059	GACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAG	1118
Qy	1239	AACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCA	1298
Db	1119	AACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCA	1178
Qy	1299	GAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAG	1358
Db	1179	GAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAG	1238
Qy	1359	AATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAA	1418
Db	1239	AATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAA	1298

Qy	1419	CTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGA	1478
Db	1299	CTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGA	1358
Qy	1479	CAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGG	1538
Db	1359	CAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGG	1418
Qy	1539	CCGGTGTGAACGCACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATTG	1598
Db	1419	CCGGTGTGAACGCACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATTG	1478
Qy	1599	TGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAG-----ACTG	1653
Db	1479	TGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGGACACAGAG	1538
Qy	1654	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1713
Db	1539	AGGCTTTGTTGTCTTTGTGGTCACCGGGTCCACTTTACACAGATGCCTATTAATCACTTC	1598
Qy	1714	TTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACATCAGATTCTG	1773
Db	1599	ACTATGGAGACAGACACATCCATCATATCACAGCAGCTCAGAAACGGGCCGTCCAGTGAA	1658
Qy	1774	ACGGCTCAAGAGGGGTATGAG-----	1794
Db	1659	AGGGGGTGAGAGGGGAAAGTGCACACTTAACCATTTGAGTTAGGTTACTGGTTGCCTGT	1718
Qy	1795	-----TCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGA	1832
Db	1719	GTCTTACACGCTTAGGGTGGTAATTGGGGTGGGGTTGCTTAAAGGCCAAACACTTTTCCC	1778
Qy	1833	CTCACCTGACAGCACAGACCCTTTGGGGGAGTGTCTTCCCATAATCACCAAGACAAGAA	1892
Db	1779	CAGACGGAGGCTCCGGTGGCCACAAGGGGGTCTGCGGAAAAGATCCCAACTGGAAGCCCA	1838
Qy	1893	GGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCTCGGCATCACCTCTT	1952
Db	1839	GAGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCTCGGCATCACCTCTT	1898
Qy	1953	GGCCATTGCAGTCATCCTGGCTTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCTGCTA	2012
Db	1899	GGCCATTGCAGTCATCCTGGCTTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCTGCTA	1958
Qy	2013	CTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCT	2072
Db	1959	CTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCT	2018
Qy	2073	CACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCCTCTTTGGGGA	2132
Db	2019	CACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCCTCTTTGGGGA	2078
Qy	2133	CACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAA	2192
Db	2079	CACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAA	2138
Qy	2193	GCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCACTGGA	2252

Db	2139	 GCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGA	2198
Qy	2253	CCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAG	2312
Db	2199	 CCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAG	2258
Qy	2313	CCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACAT	2372
Db	2259	 CCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACAT	2318
Qy	2373	GCCCCCATGGGCTCCCCTGTGATTCCACGGACCTGCCCCTGCGGGCCTCCCCAGCCA	2432
Db	2319	 GCCCCCATGGGCTCCCCTGTGATTCCACGGACCTGCCCCTGCGGGCCTCCCCAGCCA	2378
Qy	2433	CATCCCCAGCGTGGTGGTCTCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGA	2492
Db	2379	 CATCCCCAGCGTGGTGGTCTCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGA	2438
Qy	2493	CCAGCCCCAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGA	2552
Db	2439	 CCAGCCCCAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGA	2498
Qy	2553	GTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGT	2612
Db	2499	 GTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGT	2558
Qy	2613	GGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCC	2672
Db	2559	 GGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCC	2618
Qy	2673	GGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTC	2732
Db	2619	 GGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTC	2678
Qy	2733	CTACGGGGTTGACTATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGC	2792
Db	2679	 CTACGGGGTTGACTATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGC	2738
Qy	2793	CACCACTCTCAAAAAGAAACAACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCA	2852
Db	2739	 CACCACTCTCAAAAAGAAACAACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCA	2798
Qy	2853	GAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGT	2912
Db	2799	 GAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGT	2858
Qy	2913	GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGC	2972
Db	2859	 GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGC	2918
Qy	2973	CTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC	3032
Db	2919	 CTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC	2978
Qy	3033	CCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA	3092

Db 2979 CCCCAAACCATCCTTTGCTCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA 3038
Qy 3093 A 3093
|
Db 3039 A 3039

RESULT 12

AAS89721

ID AAS89721 standard; cDNA; 3039 BP.

XX

AC AAS89721;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #25525.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT; Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR P-PSDB; ABG25534.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

PS Claim 1; SEQ ID NO 25525; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The

Db	999	CTCCTTAGAAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCCTGAACTTCATCAA	1058
Qy	1179	GACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAG	1238
Db	1059	GACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAG	1118
Qy	1239	AACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCA	1298
Db	1119	AACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCA	1178
Qy	1299	GAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAG	1358
Db	1179	GAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAG	1238
Qy	1359	AATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAA	1418
Db	1239	AATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAA	1298
Qy	1419	CTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGA	1478
Db	1299	CTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGA	1358
Qy	1479	CAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGG	1538
Db	1359	CAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGG	1418
Qy	1539	CCGGTGTGAACGCACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTG	1598
Db	1419	CCGGTGTGAACGCACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTG	1478
Qy	1599	TGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAG-----ACTG	1653
Db	1479	TGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGGACACAGAG	1538
Qy	1654	ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCC	1713
Db	1539	AGGCTTTGTTGTCTTTGTGGTCACCGGGTCCACTTTACACAGATGCCTATTAATCACTTC	1598
Qy	1714	TTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTGCCAGCACAACCACATCAGATTCTG	1773
Db	1599	ACTATGGAGACAGACACATCCATCATATCACAGCAGCTCAGAAACGGGCCGTCCAGTGAA	1658
Qy	1774	ACGGCTCAAGAGGGGTATGAG-----	1794
Db	1659	AGGGGGTGAGAGGGGAAAGTGCACACTTAACCATTTTCGAGTTAGGTTACTGGTTGCCTGT	1718
Qy	1795	-----TCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGA	1832
Db	1719	GTCTTACACGCTTAGGGTGGTAATTGGGGTGGGGTGTCTTAAAGGCCAAACACTTTTCCC	1778
Qy	1833	CTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAA	1892
Db	1779	CAGACGGAGGCTCCGGTGGCCACAAGGGGGTCGTCGGAAAAGATCCCAACTGGAAGCCCA	1838
Qy	1893	GGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTT	1952

Db	1839	GAGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCTCCCGTCACCCTCTT	1898
Qy	1953	GGCCATTGCAGTCATCCTGGCTTTTCGTTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTA	2012
Db	1899	GGCCATTGCAGTCATCCTGGCTTTTCGTTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTA	1958
Qy	2013	CTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCT	2072
Db	1959	CTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCT	2018
Qy	2073	CACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGA	2132
Db	2019	CACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGA	2078
Qy	2133	CACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAA	2192
Db	2079	CACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAA	2138
Qy	2193	GCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCTGGA	2252
Db	2139	GCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCTGGA	2198
Qy	2253	CCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAG	2312
Db	2199	CCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAG	2258
Qy	2313	CCGCGGCAGCCGCGAGTGGGAGAGGAACCAAGAACCTCATCAATGCCTGCACAAAGGACAT	2372
Db	2259	CCGCGGCAGCCGCGAGTGGGAGAGGAACCAAGAACCTCATCAATGCCTGCACAAAGGACAT	2318
Qy	2373	GCCCCCATGGGCTCCCCCTGTGATTCCCACGGACCTGCCCCCTGCGGGCCTCCCCAGCCA	2432
Db	2319	GCCCCCATGGGCTCCCCCTGTGATTCCCACGGACCTGCCCCCTGCGGGCCTCCCCAGCCA	2378
Qy	2433	CATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGA	2492
Db	2379	CATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGA	2438
Qy	2493	CCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGA	2552
Db	2439	CCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGA	2498
Qy	2553	GTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGT	2612
Db	2499	GTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGT	2558
Qy	2613	GGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCC	2672
Db	2559	GGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCC	2618
Qy	2673	GGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTC	2732
Db	2619	GGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTC	2678
Qy	2733	CTACGGGGTTGACTATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGC	2792
Db	2679	CTACGGGGTTGACTATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGC	2738

Qy 2793 CACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCA 2852
 |||
 Db 2739 CACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCA 2798
 Qy 2853 GAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGT 2912
 |||
 Db 2799 GAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCGCCGAGAGGGTGGACTCCATCCAGGT 2858
 Qy 2913 GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGC 2972
 |||
 Db 2859 GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGC 2918
 Qy 2973 CTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC 3032
 |||
 Db 2919 CTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC 2978
 Qy 3033 CCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA 3092
 |||
 Db 2979 CCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA 3038
 Qy 3093 A 3093
 |
 Db 3039 A 3039

RESULT 13

AAH17625

ID AAH17625 standard; cDNA; 3041 BP.

XX

AC AAH17625;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human cDNA sequence SEQ ID NO:17153.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

Qy	1210	TCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAAAATT	1269
Db	301	TCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAAAATT	360
Qy	1270	GCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTCTGGGATCAGAG	1329
Db	361	GCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTCTGGGATCAGAG	420
Qy	1330	AAGGGAATCATCTTGAAGTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGC	1389
Db	421	AAGGGAATCATCTTGAAGTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGC	480
Qy	1390	CTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAA	1449
Db	481	CTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGATGGAGTCGAA	540
Qy	1450	GACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTC	1509
Db	541	GACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTC	600
Qy	1510	TCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAaaaaa	1569
Db	601	TCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAaaaaa	660
Qy	1570	ACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGC	1629
Db	661	ACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGC	720
Qy	1630	CATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGAT	1689
Db	721	CATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGAT	780
Qy	1690	GGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTG	1749
Db	781	GGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCTCTTG	840
Qy	1750	CCCAGCACAACCACATCAGATTTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	841	CCCAGCACAACCACATCAGATTTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	900
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	901	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	960
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	961	TCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGAC	1020
Qy	1930	CAGCTGGTTCCCGTCACCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTTCATGGGGGCC	1989
Db	1021	CAGCTGGTTCCCGTCACCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTTCATGGGGGCC	1080
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	1081	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	1140

Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	1141	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	1200
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	1201	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	1260
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	1261	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	1320
Qy	2230	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCCAACG	2289
Db	1321	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCCAACG	1380
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	1381	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	1440
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2409
Db	1441	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	1500
Qy	2410	CCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2469
Db	1501	CCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	1560
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG	2529
Db	1561	GGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG	1620
Qy	2530	GAGGACCAGGCCGCCCACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	1621	GAGGACCAGGCCGCCCACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	1680
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	1681	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	1740
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	1741	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	1800
Qy	2710	CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769
Db	1801	CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	1860
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT	2829
Db	1861	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT	1920
Qy	2830	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	2889
Db	1921	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	1980
Qy	2890	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	2949

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      |||
Db      1981 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2040
Qy      2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
      |||
Db      2041 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 2100
Qy      3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
      |||
Db      2101 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 2160
Qy      3070 AAGCCCAATGATGCGTGTACATAA 3093
      |||
Db      2161 AAGCCCAATGATGCGTGTACATAA 2184

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RESULT 14

AAA93630

ID AAA93630 standard; cDNA; 1890 BP.

XX

AC AAA93630;

XX

DT 16-JAN-2001 (first entry)

XX

DE Human semaphorin protein-like splice variant SECX pCR2.1-2864933 cDNA.

XX

KW SECX protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
 KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ss.

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OS Homo sapiens.

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PN WO200053742-A2.

XX

PD 14-SEP-2000.

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PF 09-MAR-2000; 2000WO-US006280.

XX

PR 09-MAR-1999; 99US-0123667P.

PR 08-MAR-2000; 2000US-0520781P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA;

XX

DR WPI; 2000-594318/56.

DR P-PSDB; AAB23043.

XX

PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of

PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.

XX

PS Claim 3; Fig 15; 151pp; English.

XX

CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
CC the invention are either secreted or membrane-associated proteins and act
CC as regulator of cellular proliferation and differentiation. SECX proteins
CC or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of a
CC SECX protein with other cellular proteins may be useful to modulate the
CC activity of a partner protein, cellular proliferation, cellular
CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in a
CC biological sample, and in forensic biology. SECX primers or probes are
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or
CC prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 1890 BP; 535 A; 426 C; 463 G; 466 T; 0 U; 0 Other;

Query Match 60.8%; Score 1881.6; DB 3; Length 1890;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 49 GGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAA 108
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Db 1 GGATCCGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAA 60

Qy 109 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCCACACAGAGGCACAGGCTG 168
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Db 61 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCCACACAGAGGCACAGGCTG 120

Qy 169 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 228
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 180

Qy 229 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAAGTACA 288
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAAGTACA 240

Qy 289 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 348
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Db 241 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 300

Qy	349	TGCCACAAC TTTATTAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGA	408
Db	301	TGCCACAAC TTTATTAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGA	360
Qy	409	ACTAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGG	468
Db	361	ACTAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGG	420
Qy	469	GATGAATT CAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTG	528
Db	421	GATGAATT CAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTG	480
Qy	529	TTTGCAGATGGAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTC	588
Db	481	TTTGCAGATGGAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTC	540
Qy	589	ATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGG	648
Db	541	ATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGG	600
Qy	649	TTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTC	708
Db	601	TTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTC	660
Qy	709	AGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAG	768
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Qy	769	GTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTC	828
Db	721	GTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTC	780
Qy	829	CTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTC	888
Db	781	CTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTC	840
Qy	889	CAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCT	948
Db	841	CAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCT	900
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Db	901	ACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCC	960
Qy	1009	AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTT	1068
Db	961	AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTT	1020
Qy	1069	CCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAA	1128
Db	1021	CCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAA	1080
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Db	1081	AGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCG	1140
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Db	1201	AGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACT	1260
Qy	1309	GTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAAT	1368
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Qy	1369	AGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAA	1428
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Db	1381	TGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGC	1440
Qy	1489	AGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAA	1548
Db	1441	AGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAA	1500
Qy	1549	CGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATA	1608
Db	1501	CGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATA	1560
Qy	1609	AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC	1668
Db	1561	AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC	1620
Qy	1669	ATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT	1728
Db	1621	ATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT	1680
Qy	1729	GGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGG	1788
Db	1681	GGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGG	1740
Qy	1789	TATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACA	1848
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Qy	1849	GACCCTTTGGGGGCAGTGTCTTCCCATTAATCACCAAGACAAGAAGGGAGTGATTCGGGAA	1908
Db	1801	GACCCTTTGGGGGCAGTGTCTTCCCATTAATCACCAAGACAAGAAGGGAGTGATTCGGGAA	1860
Qy	1909	AGTTACCTCAAAGGCCACGACCAGCTGG	1936
Db	1861	AGTTACCTCAAAGGCCACGACCAGCTCG	1888

RESULT 15

ADA23359

ID ADA23359 standard; cDNA; 1890 BP.

XX

AC ADA23359;

XX
DT 20-NOV-2003 (first entry)
XX
DE cDNA encoding human SECX polypeptide, SEC3 #2.
XX
KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelle WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23360.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Page 7; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.

XX

SQ Sequence 1890 BP; 535 A; 426 C; 463 G; 466 T; 0 U; 0 Other;

Query Match 60.8%; Score 1881.6; DB 8; Length 1890;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      49 GGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAA 108
      || | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGATCCGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAA 60

Qy     109 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTG 168
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTG 120

Qy     169 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 228
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 180

Qy     229 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACA 288
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACA 240

Qy     289 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 348
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Db     241 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 300

Qy     349 TGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAACGATGATGCATTGTTTGTCTGTGGA 408
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Db     301 TGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAACGATGATGCATTGTTTGTCTGTGGA 360

Qy     409 ACTAATGCCTTCAACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGG 468
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 ACTAATGCCTTCAACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGG 420

Qy     469 GATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTG 528
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Qy     589 ATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGG 648
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Qy     709 AGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAG 768
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Qy     769 GTTTGTAAGAAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTT 828
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Db	781	CTGAAGGCGCGCTTGAAC TGCTCAGTTCCTGGAGACTCTCATTTTTATTTC AACATTCTC	840
Qy	889	CAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCT	948
Db	841	CAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCT	900
Qy	949	ACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCC	1008
Db	901	ACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCC	960
Qy	1009	AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAAGTT	1068
Db	961	AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAAGTT	1020
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Db	1021	CCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAA	1080
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Qy	1369	AGTGGTTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAA	1428
Db	1321	AGTGGTTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAA	1380
Qy	1429	TGCAGCTATGATGGAGTCTGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGC	1488
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Qy	1549	CGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATA	1608
Db	1501	CGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATA	1560
Qy	1609	AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC	1668
Db	1561	AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC	1620

Qy	1669	ATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT	1728
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Qy	1909	AGTTACCTCAAAGGCCACGACCAGCTGG	1936
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Perfect score: 3093
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	657.4	21.3	1923	4	US-09-653-274-12			Sequence 12, Appl
	3	657.4	21.3	3261	4	US-09-653-274-5			Sequence 5, Appli
	4	657.4	21.3	3694	4	US-09-653-274-3			Sequence 3, Appli
c	5	604	19.5	846	4	US-09-833-381-920			Sequence 920, App
	6	555.4	18.0	3524	4	US-09-077-940A-3			Sequence 3, Appli
	7	546.8	17.7	3692	4	US-09-077-940A-1			Sequence 1, Appli
	8	443.6	14.3	2790	4	US-09-254-594-5			Sequence 5, Appli
	9	443.6	14.3	3432	4	US-09-254-594-4			Sequence 4, Appli
	10	369.8	12.0	2787	4	US-09-254-594-2			Sequence 2, Appli
	11	369.8	12.0	3195	4	US-09-254-594-1			Sequence 1, Appli

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13	252.6	8.2	4286	4	US-09-976-594-632	Sequence 632, App
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15	166	5.4	2854	1	US-08-121-713D-57	Sequence 57, Appl
16	166	5.4	2854	1	US-08-835-268-57	Sequence 57, Appl
17	166	5.4	2854	2	US-09-060-692-57	Sequence 57, Appl
18	166	5.4	2854	3	US-08-833-391-57	Sequence 57, Appl
19	166	5.4	2854	4	US-09-060-610-57	Sequence 57, Appl
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ALIGNMENTS

RESULT 1

US-09-976-594-1002

; Sequence 1002, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 1002

; LENGTH: 2278

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 411373.7
US-09-976-594-1002

Query Match 64.6%; Score 1998; DB 4; Length 2278;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
        |||
Db      281 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 340

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
        |||
Db      341 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 400

Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
        |||
Db      401 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 460

Qy     181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
        |||
Db      461 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 520

Qy     241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
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Db      521 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 580

Qy     301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 360
        |||
Db      581 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 640

Qy     361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
        |||
Db      641 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 700

Qy     421 AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
        |||
Db      701 AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 760

Qy     481 GGAATGGCCAGATGCCCATATGATGCCAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
        |||
Db      761 GGAATGGCCAGATGCCCATATGATGCCAACATGCCAACGTTGCACTGTTTGCAGATGGA 820

Qy     541 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Db      821 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 880

Qy     601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
        |||
Db      881 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 940

Qy     661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Db	941	TACTTTGTTC AAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	1000
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	1001	GTGGAGTATAACACCATGGGAAAGGTAGTTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	1060
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	1061	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	1120
Qy	841	TTGAAGTGTCTCAGTTCCTGGAGACTCTCATTTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1121	TTGAAGTGTCTCAGTTCCTGGAGACTCTCATTTTTTATTTCAACATTCTCCAGGCAGTTACA	1180
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1181	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1240
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1241	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1300
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1301	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1360
Qy	1081	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1361	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1420
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1421	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1480
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1481	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1540
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1541	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1600
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1601	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1660
Qy	1381	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1661	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1720
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1721	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1780
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1781	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1840

Qy	1561	TGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1841	TGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1900
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1901	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1960
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1961	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	2020
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	2021	TCCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG	2080
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2081	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2140
Qy	1861	GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAA	1920
Db	2141	GCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAA	2200
Qy	1921	GGCCACGACCAGCTGGTTCCTCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2201	GGCCACGACCAGCTGGTTCCTCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	2260
Qy	1981	ATGGGGGCCGTCTTCTCG	1998
Db	2261	ATGGGGGCCGTCTTCTCG	2278

RESULT 2

US-09-653-274-12

; Sequence 12, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 1923

Db 655 TTCTTCTTTTCGAGAAATCGCTGTGCGAACATAATAATTTAGGCAAGGCTGTGTATTCCCCG 714
 Qy 760 GTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGG 819
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 Db 715 GTGGCCCGCATATGTAAAAACGACATGGGTGGTTCCTCCAGCGGGTCCTGGAGAAACACTGG 774
 Qy 820 ACGTCGTTTCCTGAAGGCGCGCTTGAAGTGTCTCAGTTCCTGGAGACTCTCATTTTTTATTTT 879
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 Db 775 ACTTCATTTCTAAAGGCTCGGCTGAAGTGTCTGTCCCTGGAGATCCGTTTTTCTACTTT 834
 Qy 880 AACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCA 939
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 Db 835 GATGTTCTGCAGTCTATTACAGACATAATACAAATCAATGGCATCCCCACTGTGGTCGGG 894
 Qy 940 ACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTT 999
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 Db 895 GTGTTTACCACGCAGCTCAATAGCATCCCTGGTCTGTCTGTCTGTGCATTTAGCATGGAT 954
 Qy 1000 GACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGG 1059
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 Db 955 GACATTGAAAAAGTATTCAAAGGACGGTTTAAAGGAACAGAAACTCCAGATTCTGTTTGG 1014
 Qy 1060 ACACCAGTTCCTGATGAACGAGTTCTTAAGCCAGGCCAGGTTGCTGTGCTGGCTCATCC 1119
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 Db 1015 ACAGCAGTTCCTGAAGACAAAGTGCCAAAGCCAAGGCCTGGCTGTTGTGCAAAACACGGC 1074
 Qy 1120 TCCTTAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAG 1179
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 Db 1075 CTTGCCGAAGCTTATAAAACCTCCATCGATTTCCTGGATGAAACTCTGTCAATTCATCAA 1134
 Qy 1180 ACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGA 1239
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 Db 1135 TCTCATCCCCTGATGGACTCTGCCGTTCACCCATTGCCGATGAGCCCTGGTTCACAAAG 1194
 Qy 1240 ACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAG 1299
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 Db 1195 ACTCGGTCAGGTACAGACTGACGGCCATCTCAGTGGACCATTGAGCCGACCCTACCAG 1254
 Qy 1300 AATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGA 1359
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 Db 1255 AACTACACAGTCATCTTTGTTGGCTCTGAAGCTGGCATGGTACTTAAAGTTCTGGC---A 1311
 Qy 1360 ATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAAC 1419
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 Db 1312 AAGACCAGTCCTTTCTCTTTGAACGACAGCGTATTACTGGAAGAGATTGAAGCCTACAAC 1371
 Qy 1420 TCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGAC 1479
 || ||| |||| || | ||||| || ||||| || |||||
 Db 1372 CATGCAAAGTGCAGTGTGAGAATGAGGAAGACAAAAGGTCATCTCATTACAGTTGGAT 1431
 Qy 1480 AGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGC 1539
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 Db 1432 AAAGATCACCACGCTTTATATGTGGCGTTCTCTAGCTGCATTATCCGCATCCCCCTCAGT 1491
 Qy 1540 CGGTGTGAACGACATGGGAAGTGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGT 1599
 || |||| || ||| ||||| | ||||| || | ||||| |||||
 Db 1492 CGCTGTGAGCGTTATGGATCATGTAAAAAGTCTTGTATTGCATCTCGTGACCCGATTGT 1551

Qy 1600 GGATGGATAAAGGAAGG 1616
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 Db 1552 GGCTGGTTAAGCCAGGG 1568

RESULT 3

US-09-653-274-5

; Sequence 5, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 3261

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-653-274-5

Query Match 21.3%; Score 657.4; DB 4; Length 3261;

Best Local Similarity 64.5%; Pred. No. 2.6e-171;

Matches 1017; Conservative 0; Mismatches 551; Indels 9; Gaps 2;

Qy 40 CACTTTGCTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAAC 99
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 Db 49 CAGTTGAGGGCAGTCAGCTTTCCTGAAGATGATGAACCCCTTAATACTGTCGACTATCAC 108

Qy 100 TATACAAAACAGTATCCGGTGTGTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGG 159
 ||| ||| || ||||| ||| || | | ||| || | | |
 Db 109 TATTCAAGGCAATATCCGGTTTTTAGAGGACGCCCTTCAGG-----CAATGAATCGCAG 162

Qy 160 CACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGG 219
 ||||| ||||| | ||| |||| ||| || | || || ||||| |||
 Db 163 CACAGGCTGGACTTTCAGCTGATGTTGAAAATTCGAGACACACTTTATATTGCTGGCAGG 222

Qy 220 GACCATATTTTATACTGTTGATATAGACACATCACACGGAAGAAATTTATTGTAGCAAA 279
 || || ||||| || | || | | || | ||| | |||
 Db 223 GATCAAGTTTATACAGTAACTTAAATGAAATGCCCAAACAGAAGTAATACCCAACAAG 282

Qy 280 AAAGTACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAAATGAAGGGAAAACAT 339
 ||||| ||||| ||| |||| ||| ||| | || |||| || ||||
 Db 283 AAAGTACATGGCGATCAAGACAACAGGATCGAGAAAATGTGCTATGAAAGGCAAGCAT 342

Qy	340	AAGGATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTT	399
Db	343	AAAGATGAATGCCACAACCTTTATCAAAGTATTTGTTCCAAGAAACGATGAGATGGTTTTT	402
Qy	400	GTCTGTGGAACATAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAA	459
Db	403	GTTTGTGGTACCAATGCATTCAATCCCATGTGTAGATACTACAGGTTGAGTACCTTAGAA	462
Qy	460	CCATTTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAAC	519
Db	463	TATGATGGGGAAGAAATTAGTGGCCTGGCAAGATGCCCATTTGATGCCAGACAAACCAAT	522
Qy	520	GTTGCACTGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATT	579
Db	523	GTTGCCCTCTTTGCTGATGGGAAGCTGTATTCTGCCACAGTGGCTGACTTCTTGCCAGC	582
Qy	580	GACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGAT	639
Db	583	GATGCCGTTATTTATCGAAGCATGGGTGATGGATCTGCCCTTCGCACAATAAAATATGAT	642
Qy	640	TCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTAC	699
Db	643	TCCAAATGGATAAAAGAGCCACACTTCTTCATGCCATAGAATATGGAACTATGTCTAT	702
Qy	700	TTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCAAGA	759
Db	703	TTCTTCTTTTCGAGAAATCGCTGTGGAACATAATAATTTAGGCAAGGCTGTGTATTCCCGC	762
Qy	760	GTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGG	819
Db	763	GTGGCCCGCATATGTAAAACGACATGGGTGGTTCCCAGCGGGTCCTGGAGAAACACTGG	822
Qy	820	ACGTCGTTCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTC	879
Db	823	ACTTCATTTCTAAAGGCTCGGCTGAAGTGTCTGTCCCTGGAGATCCGTTTTTCTACTTT	882
Qy	880	AACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCTCGGCA	939
Db	883	GATGTTCTGCAGTCTATTACAGACATAATACAAATCAATGGCATCCCCACTGTGGTCGGG	942
Qy	940	ACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTT	999
Db	943	GTGTTTACCACGCAGCTCAATAGCATCCCTGGTCTGTGCTGTCTGTGCATTTAGCATGGAT	1002
Qy	1000	GACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGG	1059
Db	1003	GACATTGAAAAGTATTCAAAGGACGGTTTAAGGAACAGAAAACCTCCAGATTCTGTTTGG	1062
Qy	1060	ACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCC	1119
Db	1063	ACAGCAGTTCCTGAAGACAAAGTGCCAAAGCCAAGGCCTGGCTGTTGTGCAAAACACGGC	1122
Qy	1120	TCCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACCTCATCAAG	1179
Db	1123	CTTGCCGAAGCTTATAAAACCTCCATCGATTTCCTGGGATGAAACTCTGTCATTATCAAA	1182
Qy	1180	ACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGA	1239

Db	1183	TCTCATCCCCTGATGGACTCTGCCGTTCCACCCATTGCCGATGAGCCCTGGTTCACAAAG	1242
Qy	1240	ACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAG	1299
Db	1243	ACTCGGGTCAGGTACAGACTGACGGCCATCTCAGTGGACCATTGAGCCGGACCCTACCAG	1302
Qy	1300	AATCACACTGTGGT'TTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGA	1359
Db	1303	AACTACACAGTCATCTTTGTTGGCTCTGAAGCTGGCATGGTACTTAAAGTTCTGGC---A	1359
Qy	1360	ATAGGAAATAGTGGT'TTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGT'TTACAAC	1419
Db	1360	AAGACCAGTCCTTTTCTCTTTGAACGACAGCGTATTACTGGAAGAGATTGAAGCCTACAAC	1419
Qy	1420	TCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGAC	1479
Db	1420	CATGCAAAGTGCAGTGTGAGAATGAGGAAGACAAAAGGTCATCTCATTACAGTTGGAT	1479
Qy	1480	AGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGC	1539
Db	1480	AAAGATCACCACGCTTTATATGTGGCGTTCTCTAGCTGCATTATCCGCATCCCCCTCAGT	1539
Qy	1540	CGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGT	1599
Db	1540	CGCTGTGAGCGTTATGGATCATGTAAAAAGTCTTGTATTGCATCTCGTGACCCGTATTGT	1599
Qy	1600	GGATGGATAAAGGAAGG	1616
Db	1600	GGCTGGTTAAGCCAGGG	1616

RESULT 4

US-09-653-274-3

; Sequence 3, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 3694

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (434)..(3694)
US-09-653-274-3

Query Match 21.3%; Score 657.4; DB 4; Length 3694;
Best Local Similarity 64.5%; Pred. No. 2.8e-171;
Matches 1017; Conservative 0; Mismatches 551; Indels 9; Gaps 2;

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Qy      40  CACTTTGCTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAAC 99
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Db      482  CAGTTGAGGGCAGTCAGCTTTCCTGAAGATGATGAACCCCTTAATACTGTCGACTATCAC 541

Qy     100  TATACAAAACAGTATCCGGTGTGTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGG 159
      ||| ||| || | | | | | | | | | | | | | | | |
Db     542  TATTCAAGGCAATATCCGGTTTTTAGAGGACGCCCTTCAGG-----CAATGAATCGCAG 595

Qy     160  CACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGG 219
      || | | | | | | | | | | | | | | | | | | | |
Db     596  CACAGGCTGGACTTTCAGCTGATGTTGAAAATTCGAGACACACTTTATATTGCTGGCAGG 655

Qy     220  GACCATATTTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAA 279
      || | | | | | | | | | | | | | | | | | | | |
Db     656  GATCAAGTTTATACAGTAAACTTAAATGAAATGCCCAAAACAGAAGTAATACCCAACAAG 715

Qy     280  AAACGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACAT 339
      || | | | | | | | | | | | | | | | | | | | |
Db     716  AAACGACATGGCGATCAAGACAACAGGATCGAGAAAACGTGTCTATGAAAGGCAAGCAT 775

Qy     340  AAGGATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTT 399
      || | | | | | | | | | | | | | | | | | | | |
Db     776  AAAGATGAATGCCACAACTTTATCAAAGTATTTGTTCCAAGAAACGATGAGATGGTTTTT 835

Qy     400  GTCTGTGGAACATAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAA 459
      || | | | | | | | | | | | | | | | | | | | |
Db     836  GTTGTGGTACCAATGCATTCAATCCCATGTGTAGATACTACAGGTTGAGTACCTTAGAA 895

Qy     460  CCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAAC 519
      || | | | | | | | | | | | | | | | | | | | |
Db     896  TATGATGGGGAAGAAATTAGTGGCCTGGCAAGATGCCCATTGATGCCAGACAAACCAAT 955

Qy     520  GTTGCATGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATT 579
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Db     956  GTTGCCCTCTTTGCTGATGGGAAGCTGTATTCTGCCACAGTGGCTGACTTCTTGCCAGC 1015

Qy     580  GACGCAGTCATTTACCGGAGTCTTGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGAT 639
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Db    1016  GATGCCGTTATTTATCGAAGCATGGGTGATGGATCTGCCCTTCGCACAATAAAATATGAT 1075

Qy     640  TCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTAC 699
      || | | | | | | | | | | | | | | | | | | | |
Db    1076  TCCAAATGGATAAAAGAGCCACACTTCTTCATGCCATAGAATATGGAACTATGTCTAT 1135

Qy     700  TTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGA 759
      || | | | | | | | | | | | | | | | | | | | |
Db    1136  TTCTTCTTTTCGAGAAATCGCTGTCTGAACATAATAATTTAGGCAAGGCTGTGTATTCCCGC 1195
```

Qy 760 GTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGG 819
 ||||| | | ||||| || || ||||| || || || | ||||| ||||| ||||
 Db 1196 GTGGCCCGCATATGTAAAAACGACATGGGTGGTTCACGCGGGTCCTGGAGAAACACTGG 1255

Qy 820 ACGTCGTTCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTC 879
 || || || || ||||| || ||||| || || ||||| || || || || ||
 Db 1256 ACTTCATTTCTAAAGGCTCGGCTGAAGTGTCTGTCCCTGGAGATCCGTTTTTCTACTTT 1315

Qy 880 AACATTCTCCAGGCAGTTACAGATGTGATTCTGATCAACGGGCGTGATGTTGTCCTGGCA 939
 | |||| ||| | ||||| | || | |||| | || || || ||
 Db 1316 GATGTTCTGCAGTCTATTACAGACATAATAACAAATCAATGGCATCCCCACTGTGGTCGGG 1375

Qy 940 ACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTT 999
 |||| | || | || ||||| |||| ||||| ||||| || || |||| |
 Db 1376 GTGTTTACCACGCAGCTCAATAGCATCCCTGGTCTGCTGTCTGTGCATTTAGCATGGAT 1435

Qy 1000 GACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGG 1059
 ||||| | || || | || | || ||||| |||| |||| | ||
 Db 1436 GACATTGAAAAGTATTCAAAGGACGGTTTAAGGAACAGAAACTCCAGATTCTGTTTGG 1495

Qy 1060 ACACCAAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCC 1119
 || ||||| || || || || || ||||| |||| || || || || ||
 Db 1496 ACAGCAGTTCCTGAAGACAAAGTGCCAAAGCCAAGGCTGGCTGTTGTGCAAAACACGGC 1555

Qy 1120 TCCTTAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAG 1179
 ||| ||| ||||| || ||||| |||| || ||| ||||| ||
 Db 1556 CTTGCCGAAGCTTATAAAACCTCCATCGATTTCCTGGATGAAACTCTGTCAATTCATCAA 1615

Qy 1180 ACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCTGAGA 1239
 | || || || ||||| || || || |||| | | || ||||| |
 Db 1616 TCTCATCCCCTGATGGACTCTGCCGTTCCACCCATTGCCGATGAGCCCTGGTTCACAAAG 1675

Qy 1240 ACAATGGTCAGATACCGCCTTACCAAATTCAGTGGACACAGCTGCTGGGCCATATCAG 1299
 || ||||| ||| | || || || ||||| || || || || || || ||
 Db 1676 ACTCGGGTCAGGTACAGACTGACGGCCATCTCAGTGGACCATTGAGCCGACCCTACCAG 1735

Qy 1300 AATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGA 1359
 || |||| || || || || || || || || || || || || || || ||
 Db 1736 AACTACACAGTCATCTTTGTTGGCTCTGAAGCTGGCATGGTACTTAAAGTTCTGGC---A 1792

Qy 1360 ATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAAC 1419
 | | | | | ||||| || ||||| |||| | ||||| |||||
 Db 1793 AAGACCAGTCCTTTCTCTTTGAACGACAGCGTATTACTGGAAGAGATTGAAGCCTACAAC 1852

Qy 1420 TCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGAC 1479
 || ||| |||| ||| | ||||| |||| | |||| | ||| ||||
 Db 1853 CATGCAAAGTGCAGTGCTGAGAATGAGGAAGACAAAAAGGTCATCTCATTACAGTTGGAT 1912

Qy 1480 AGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGC 1539
 | || | | || || ||||| ||||| || || | |||| |
 Db 1913 AAAGATCACCACGCTTTATATGTGGCGTTCTCTAGCTGCATTATCCGCATCCCCCTCAGT 1972

Qy 1540 CGGTGTGAACGACATGGGAAGTGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGT 1599
 || |||| || |||| ||||| ||||| || ||||| ||||| |||||
 Db 1973 CGCTGTGAGCGTTATGGATCATGTAAAAAGTCTTGTATTGCATCTCGTGACCCGTATTGT 2032

Qy 1600 GGATGGATAAAGGAAGG 1616

Db 2033 GGCTGGTTAAGCCAGGG 2049

RESULT 5

US-09-833-381-920/c
; Sequence 920, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-920

Query Match 19.5%; Score 604; DB 4; Length 846;
Best Local Similarity 100.0%; Pred. No. 6.9e-157;
Matches 604; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC	60
Db	604	ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC	545
Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	120
Db	544	CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG	485
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	484	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	425
Qy	181	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	424	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	365
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	364	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	305
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	360
Db	304	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	245
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	244	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	185
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480


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          |||
Db      184 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 125
Qy      481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
          |||
Db      124 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 65
Qy      541 AAACATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
          |||
Db      64 AAACATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 5
Qy      601 CTTG 604
          |||
Db      4 CTTG 1

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RESULT 6

US-09-077-940A-3

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; Sequence 3, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(38)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2706)..(3524)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (39)..(2702)
; OTHER INFORMATION:
US-09-077-940A-3

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Query Match      18.0%; Score 555.4; DB 4; Length 3524;
Best Local Similarity 60.0%; Pred. No. 4.3e-143;
Matches 1026; Conservative 0; Mismatches 656; Indels 27; Gaps 5;

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Qy      13 GCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTCCAGAAAGATTCT 72
          ||| ||||| | || | || | || | || |
Db      72 GCCCTGCTGCTTCTGCTGCTGCTACTGGGGGGCGCCACGGCTCTTTCCTGAGGACCCG 131
Qy      73 GAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTGTTTGTGGGGCCAC 132
          ||| | || | || | || | || | ||| ||||| ||||| |||
Db      132 CCGCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCACTATCCCGTGTTTGTGGGCAGC 191
Qy      133 AAGCCAGGACGGAACACCAC-----ACAGAGGCACAGGCTGGACATCCAGATGATTATG 186

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Db	192	GGGCCCCGACGCCTGACCCCCGAGAAGGTGCTGACGACCTCAACATCCAGCGAGTCTCTG	251
Qy	187	ATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGATATAGAC	246
Db	252	CGGGTCAACAGGACGCTGTTTCATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAG	311
Qy	247	ACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGACAGGCC	306
Db	312	CCCCCAGCTCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGC	371
Qy	307	GATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTTATTAAA	366
Db	372	GACATAAACGTGTGTGCGGATGAAGGGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAG	431
Qy	367	GTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAATAATGCCTTCAACCCCT	426
Db	432	GTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGCGGTTCCAACGCTTCAACCCG	491
Qy	427	TCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAAGCGGAATG	486
Db	492	GTGTGCGCCAACCTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGCGGTATG	551
Qy	487	GCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGAAAACTA	546
Db	552	GCCCCGTGCCCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTC	611
Qy	547	TACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGTCTTGGA	606
Db	612	TTCACAGTACTGTTACCGACTTCCTAGCCATTGATGCTGTCATCTACCGAGCCTCGGG	671
Qy	607	GAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCATACTTT	666
Db	672	GACAGGCCCAACCCTGCGCACCGTGAAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTT	731
Qy	667	GTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCCAGGGAAATAGCAGTGGAG	726
Db	732	GTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTCTTCCGGGAGATTGCGATGGAG	791
Qy	727	TATAACACCATGGGAAAGGTAGTTTTCCTCAAGAGTGGCTCAGGTTTGTGAAGATGATATG	786
Db	792	TTTAACTACCTGGAGAAGGTGGTGGTGTCCGCGTGGCCCGAGTGTGCAAGAACGACGTG	851
Qy	787	GGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGCTTGAAC	846
Db	852	GGAGGCTCCCCCGCGTGCTGGAGAAGCAGTGGACGTCCTTCCTGAAGGCGCGGCTCAAC	911
Qy	847	TGCTCAGTTCCTGGAGACTCTCATTTTATTTCAACATTCTCCAGGCAGTTACAGATGTG	906
Db	912	TGCTCTGTACCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTCACGGGCGTG	971
Qy	907	ATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTCTACACCTTATAACAGCATC	966
Db	972	GTCAGCCTCGGGGGCCGGCCCGTGGTCTGGCCGTTTTTCCACGCCAGCAACAGCATC	1031
Qy	967	CCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGA	1026

Db 1032 CCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTGGCAGCTGTGTTTGAAGGCCGC 1091
 Qy 1027 TTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCT 1086
 ||| || ||||| || || ||| ||||| || || || || || || ||
 Db 1092 TTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAGGTGCCT 1151
 Qy 1087 AAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCTCCTTAGAAAGATATGCAACCTCCAAT 1146
 ||| ||| || ||| || || || || || || || || || || || ||
 Db 1152 CGACCCCGGCCCGGGTGCT-----GCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGC 1205
 Qy 1147 GAGTTCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTG 1206
 | || || ||||| | || ||||| ||||| ||||| || ||||| ||||| ||
 Db 1206 GCCTTGCCGGATGACATCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTG 1265
 Qy 1207 CCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAA 1266
 ||||| | | | ||| ||| ||||| | || || | || ||| || || |
 Db 1266 CCCTCGCTGGGCCATGCGCCCTGGATCCTGCGGACCCTGATGAGGCACCAGCTGACTCGA 1325
 Qy 1267 ATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCA 1326
 | || ||||| | || || || | || || || || || || || || || ||
 Db 1326 GTGGCTGTGGACGTGGGAGCCGGCCCTGGGGCAACCAGACCGTTGTCTTCTGGGTTCT 1385
 Qy 1327 GAGAAGGGAATCATCTTGAAGTTTTT-----GGCCAGAATAGGAAATAGTGGTTTTCTA 1380
 ||| ||| | | | ||||| | | ||| | | | | | ||
 Db 1386 GAGGCGGGGACGGTCTCAAGTTCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT 1445
 Qy 1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAG-----C 1434
 ||| | ||||| ||||| | ||| | || | || | || |
 Db 1446 GGGCTCAGTGTCTTCCTGGAGGAGTTTGAGACCTACCGGCCGGACAGGTGTGGACGGCCC 1505
 Qy 1435 TATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCT 1494
 | ||| | || | || | || || || ||||| ||| |
 Db 1506 GCGGCTGGCGAGACAGGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGC 1565
 Qy 1495 CTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGCCCGGTGTGAACGACAT 1554
 ||| ||| ||| ||| ||| ||| || || || || || || || || ||
 Db 1566 CTGCTGGCTGCCTTCCCCGCTGCGTGGTCCGAGTGCCTGTGGCTCGCTGCCAGCAGTAC 1625
 Qy 1555 GGGAAGTGTAACAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAA 1614
 | |||| || | ||||| | | |||| || || || || || || ||
 Db 1626 TCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGCGGGTGGGCCCCCGAC 1685
 Qy 1615 GGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAG 1674
 || ||||| | | || || |||| | ||||| ||||| ||
 Db 1686 GGCT---CCTGCATCTTCCTCAGCCCGGGCACCAGAGCCGCCTTTGAGCAGGACGTGTCC 1742
 Qy 1675 CGTGGCAATACAGATGGTCTGGGGGACTG 1703
 | || || || || | ||||| ||
 Db 1743 GGGGCCAGCACCTCAGGCTTAGGGGACTG 1771

RESULT 7

US-09-077-940A-1

; Sequence 1, Application US/09077940A

; Patent No. 6576441

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru et al.

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; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3692
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(18)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (19)..(2682)
; OTHER INFORMATION:
; NAME/KEY: 3'UTR
; LOCATION: (2683)..(3653)
; OTHER INFORMATION:
; NAME/KEY: polyA_site
; LOCATION: (3654)..(3692)
; OTHER INFORMATION:
US-09-077-940A-1
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Query Match          17.7%; Score 546.8; DB 4; Length 3692;
Best Local Similarity 60.3%; Pred. No. 1.1e-140;
Matches 1006; Conservative 0; Mismatches 632; Indels 30; Gaps 5;
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Qy      57 TTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCC 116
      ||||| || | ||| |||| | | | | ||| | || || ||
Db      99 TTTCCCAGATGAACCACCTCCACTCAGTGTGGCTCCCAGGGACTACCTGAGCCACTACCC 158

Qy     117 GGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGC-----ACAGGCTGGA 170
      ||||| ||||| | ||| || || ||| | | | | || ||
Db     159 CGTGTTCGTGGGCAGCGGGCCTGGTTCGTCTGACCCCTGCAGAGGGTGCTGAGGACCTCAA 218

Qy     171 CATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTA 230
      ||||| || | | ||| || || || || || | | || || || ||
Db     219 CATCCAGAGAGTGCTACGTGTAAACAGGACACTGTTTCATCGGGACAGAGACAACCTGTA 278

Qy     231 TACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATG 290
      || || | || |||| | || | | | || || || || ||
Db     279 CCAAGTAGAACTGGAGCCATCCACATCCACGGAGCTGCGGTATCAGCGGAAGCTTACCTG 338

Qy     291 GAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTG 350
      | || | | || | || || | ||||| || || || |||||
Db     339 GCGCTCCAACCCAGTGACATCGATGTGTGTCGGATGAAGGGCAAGCAAGAGGGTGAGTG 398

Qy     351 CCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAAC 410
      | ||||| | || || || || |||| | | || || || ||
Db     399 TCGGAACTTTGTCAAGGTGCTCCTGCTTCGTGACGAATCCACGCTCTTCGTGTGCGGCTC 458

Qy     411 TAATGCCTTCAACCCCTTCTCGCAGAACTATAAGATGGATAACATTGGAACCATTCGGGGA 470
      ||||| ||||| || ||| || || | |||| ||| || | | || ||
Db     459 CAATGCATTCAATCCCATCTGTGCCAATTACAGTATGGACACACTGCAGCTTCTTGGAGA 518
```

Qy 471 TGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTT 530
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 519 CAACATCAGTGGTATGGCCCCTGCCCCACGACCCCAAGCATGCCAATGTCGCCCTCTT 578

Qy 531 TGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCGAGTCAT 590
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 579 CTCAGATGGGATGCTCTTCACAGCCACAGTAACTGACTTCCTAGCCATCGACGCTGTTAT 638

Qy 591 TTACCGGAGTCTTGAGAAAGCCCTACCCGCGGACCGTCAAGCACGATTCAAATGGTT 650
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 639 CTACCGTAGCCTTGGGGACCGGCCACACTGCGCACAGTAAAGCATGACTCCAAGTGGTT 698

Qy 651 GAAAGAACCATACTTTGTTCAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAG 710
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 699 TAAAGAGCCATACTTTGTGCATGCGGTGGAGTGGGGAAGCCACGTCTACTTCTTCTCCG 758

Qy 711 GGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGT 770
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 759 GGAGATCGCCATGGAGTTTAACTATCTGGAAAGGTGGTGGTGTCCCGTGTGGCCCGTGT 818

Qy 771 TTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCT 830
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 819 ATGCAAGAATGATGTGGGCGGCTCCCCACGGGTGCTGGAGAAGCAGTGGACTTCTTCCT 878

Qy 831 GAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCA 890
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 879 GAAGGCCCGGCTCAACTGCTCCGTGCCTGGGGACTCACACTTCTACTTCAATGTACTGCA 938

Qy 891 GGCAGTTACAGATGTGATTCTGATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTAC 950
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 939 GGCTGTGACTGGTGTGGTGAGCCTTGCGGCCGTCCAGTGATTCTTGCTGTCTTCTCAAC 998

Qy 951 ACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAG 1010
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 999 TCCTAGCAACAGCATCCCTGGCTCAGCTGTCTGTGCCTTTGACATGAACCAAGTGGCTGC 1058

Qy 1011 TGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCC 1070
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1059 TGTGTTTGAAGGCCGCTTCCGGGAGCAGAAGTCACCTGAGTCAATCTGGACCCAGTGCC 1118

Qy 1071 TGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCTCCTTAGAAAG 1130
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1119 TGAGGACCAAGTACCACGGCCCAGGCCGGGTGCTGTG-----CAGCGCCCGGTATGCA 1172

Qy 1131 ATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCT 1190
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1173 GTACAACGCATCCAATGCCCTTCCTGACGAGATTCTCAACTTTGTAAAGACCCACCCACT 1232

Qy 1191 CATGGATGAGGCAGTGGCCTCCATCTTCAACAGGCCATGGTTCCCTGAGAACAATGGTCAG 1250
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1233 GATGGACGAAGCGGTGCCCTCCCTGGGCCACTCGCCTTGATTGTGAGAACTCTGATACG 1292

Qy 1251 ATACCGCCTTACCAAATTCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGT 1310
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1293 GCACCAGCTGACCCGAGTGGCTGTGGATGTGGGTGCAGGCCCATGGGGCAATCAGACAAT 1352

Qy 1311 GGTTTTTCTGGGATCAGAGAAGGAATCATCTTGAAGTTTTT-----GGCCAGAATAGG 1364

Query Match 14.3%; Score 443.6; DB 4; Length 2790;
Best Local Similarity 58.6%; Pred. No. 3.1e-112;
Matches 849; Conservative 0; Mismatches 584; Indels 15; Gaps 4;

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Qy      164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACC 223
          ||||| | | | | | | | | | | | | | | | | | | | | | |
Db      179 GGCTGGACTTTCAGAGATTCCTGACCTTGAACCGGACCTTGCTAGTGGCTGCCCCGGGATC 238

Qy      224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
          | | | | | | | | | | | | | | | | | | | | | |
Db      239 ACGTTTTTCTCCTTCGATCTTCAAGCCGAAGAAGAGGGGAGGGGCTGGTGCCCAACAAGT 298

Qy      284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
          | | | | | | | | | | | | | | | | | | | | | |
Db      299 ATCTA---ACATGGAGAAGCCAAGATGTGGAGAACTGTGCTGTACGGGGAAAGCTGACGG 355

Qy      344 ATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
          ||||| | | | | | | | | | | | | | | | | | | |
Db      356 ATGAGTGCTACAACATATTCGTGTTCTTGTTCCTGGGACTCCCAGACGCTCCTTGCCT 415

Qy      404 GTGGAACATAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCAT 463
          ||||| | | | | | | | | | | | | | | | | | | |
Db      416 GTGGAACGAACATTCAGCCCTGTGTGCCGAGCTATGGGATAACTTCGCTGCAGCAGG 475

Qy      464 TCGGGGATGAATTAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
          || | | | | | | | | | | | | | | | | | | | | |
Db      476 AGGGTGAGGAAGTGAAGTGGGCGAGGCTCGATGCCCTTTGATGCCACCCAGTCCAACGTGG 535

Qy      524 CACTGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACG 583
          | | | | | | | | | | | | | | | | | | | | | |
Db      536 CCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGGCCAGTGATG 595

Qy      584 CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAA 643
          | | | | | | | | | | | | | | | | | | | | | |
Db      596 CTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCACTCCGCTCCGCCAAGTATGACTCCA 655

Qy      644 AATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCT 703
          | | | | | | | | | | | | | | | | | | | | | |
Db      656 AGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATGTCTACTTCT 715

Qy      704 TCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGG 763
          ||||| | | | | | | | | | | | | | | | | | | |
Db      716 TCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAGTTCTCCCGCGTAG 775

Qy      764 CTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGT 823
          | | | | | | | | | | | | | | | | | | | | | |
Db      776 CCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTCGGGCCTTGGACCGCCACTGGACAT 835

Qy      824 CGTTCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACA 883
          | | | | | | | | | | | | | | | | | | | | | |
Db      836 CCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGACTCTACTTTCTATTTTGATG 895

Qy      884 TTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGT 943
          || | | | | | | | | | | | | | | | | | | | | |
Db      896 TTTTACAGGCCTTGAAGTGGGCTGTGAACCTGCATGGCCGCTCTGCTCTCTTTGGGGTCT 955

Qy      944 TTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACA 1003
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Db	956	TCACCACCCAGACCAATAGCATCCCTGGCTCTGCCGTCTGCGCCTTCTACCTGGATGAGA	1015
Qy	1004	TTGCCAGTGTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACAC	1063
Db	1016	TTGAGCGTGGGTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGGATGGGGCCTGGACTC	1075
Qy	1064	CAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCT	1123
Db	1076	CTGTGTCTGAGGACAGAGTTCCTCACCCAGGCCAGGATCCTGTGCAGGAGTAGGGGGAG	1135
Qy	1124	TAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGC	1183
Db	1136	CTGCCTTGTCTCCTCTTCCCGAGACCTCCCTGATGATGTCTGACCTTCATCAAGGCTC	1195
Qy	1184	ACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAA	1243
Db	1196	ACCCGCTGCTGGACCCCGCTGTACCACCTGTCACCCATCAGCC---TCTACTCACTCTCA	1252
Qy	1244	TGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATC	1303
Db	1253	CTAGCAGGGCCCTACTGACCCAAGTAGCTGTGGATGGCATGGCTGGTCCCCACAGTAACA	1312
Qy	1304	ACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAG	1363
Db	1313	TCACAGTCATGTTCCCTGGCTCCAATGATGGGACAGTGCTGAAGGTGCTGACCCAGGTG	1372
Qy	1364	GAAATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTG	1423
Db	1373	GGCGATCCGG---GGGACCTGAGCCCATCCTCCTGGAAGAGATTGATGCCTACAGCCCTG	1429
Qy	1424	AAAAATGCAGCTATGATGGAGTCG-----AAGACAAAAGGATCATGGGCATGCAGCTGG	1477
Db	1430	CCCGGTGCAGTGGGAAGCGGACAGCCCAAACAGCACGACGATCATAGGGCTGGAGCTGG	1489
Qy	1478	ACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTG	1537
Db	1490	ACACTGAGGGTCACAGGCTTTTTGTGGCTTTTTCTGGCTGTATTGTCTACCTCCCTCTCA	1549
Qy	1538	GCCGGTGTGAACGACATGGGAAGTGTAACCACTGTATTGCCTCCAGAGACCCATATT	1597
Db	1550	GCCGGTGTGCCCCGGCATGGGGCCTGTCAGAGGAGCTGTTTGGCTTCTCAGGACCCATACT	1609
Qy	1598	GTGGATGG-1605	
Db	1610	GTGGATGG 1617	

RESULT 9

US-09-254-594-4

; Sequence 4, Application US/09254594

; Patent No. 6566094

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru

; APPLICANT: KIKUCHI, Kaoru

; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y

; FILE REFERENCE: 0020-4527P


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; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: ' 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: 5'UTR
; LOCATION: (1)..(187)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc_feature
; LOCATION: (188)..(2977)
; OTHER INFORMATION: CDS; Identification Method: E
; NAME/KEY: 3'UTR
; LOCATION: (2978)..(3407)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: polyA_signal
; LOCATION: (3408)..(3432)
; OTHER INFORMATION: Identification Method: E
US-09-254-594-4

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Query Match          14.3%; Score 443.6; DB 4; Length 3432;
Best Local Similarity 58.6%; Pred. No. 3.5e-112;
Matches 849; Conservative 0; Mismatches 584; Indels 15; Gaps 4;

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Qy      164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACC 223
        ||||| | | | | | | | | | | | | | | | | | | | | | |
Db      366 GGCTGGACTTTCAGAGATTCCTGACCTTGAACCGGACCTTGCTAGTGGCTGCCGGGATC 425

Qy      224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
        | | | | | | | | | | | | | | | | | | | | | |
Db      426 ACGTTTTCTCCTTCGATCTCAAGCCGAAGAAGAAGGGGAGGGGCTGGTGCCCAACAAGT 485

Qy      284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
        | | | | | | | | | | | | | | | | | | | | | |
Db      486 ATCTA--ACATGGAGAAGCCAAGATGTGGAGAACTGTGCTGTACGGGGAAAGCTGACGG 542

Qy      344 ATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
        ||||| | | | | | | | | | | | | | | | | | | |
Db      543 ATGAGTGCTACAACATATATTCGTGTTCTTGTTCCTGGGACTCCCAGACGCTCCTTGCCT 602

Qy      404 GTGGAACATAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCAT 463
        ||||| | | | | | | | | | | | | | | | | | | |
Db      603 GTGGAACGAACATTCAGCCCTGTGTGCCGCAGCTATGGGATAACTTCGCTGCAGCAGG 662

Qy      464 TCGGGGATGAATTTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
        || | | | | | | | | | | | | | | | | | | | | |
Db      663 AGGGTGAGGAAGTGAAGTGGGCAGGCTCGATGCCCTTTGATGCCACCCAGTCCAACGTGG 722

Qy      524 CACTGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACG 583
        | | | | | | | | | | | | | | | | | | | | | |
Db      723 CCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGGCCAGTGATG 782

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Qy	584	CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCTGCGGACCGTCAAGCACGATTCAA	643
Db	783	CTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCACTCCGCTCCGCCAAGTATGACTCCA	842
Qy	644	AATGGTTGAAAGAACCATACTTTGTTCAGCCGTGGATTACGGAGATTATATCTACTTCT	703
Db	843	AGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATGTCTACTTCT	902
Qy	704	TCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGG	763
Db	903	TCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAGTTCTCCGCGTAG	962
Qy	764	CTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGT	823
Db	963	CCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTCGGGCCTTGGACCGCCACTGGACAT	1022
Qy	824	CGTTCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACA	883
Db	1023	CCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCTATTTTGATG	1082
Qy	884	TTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGT	943
Db	1083	TTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCTTTGGGGTCT	1142
Qy	944	TTTCTACACCTTATAACAGCATCCCTGGGTCTGCACTCTGTGCCTATGACATGCTTGACA	1003
Db	1143	TCACCACCCAGACCAATAGCATCCCTGGCTCTGCCGTCTGCGCCTTCTACCTGGATGAGA	1202
Qy	1004	TTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACAC	1063
Db	1203	TTGAGCGTGGGTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGGATGGGGCCTGGACTC	1262
Qy	1064	CAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCT	1123
Db	1263	CTGTGTCTGAGGACAGAGTTCCTCACCCAGGCCAGGATCCTGTGCAGGAGTAGGGGGAG	1322
Qy	1124	TAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGC	1183
Db	1323	CTGCCTTGTCTCCTCTTCCCGAGACCTCCCTGATGATGTCTGACCTTCATCAAGGCTC	1382
Qy	1184	ACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAA	1243
Db	1383	ACCCGCTGCTGGACCCCGCTGTACCACCTGTCACCCATCAGCC---TCTACTACTCTCA	1439
Qy	1244	TGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATC	1303
Db	1440	CTAGCAGGGCCCTACTGACCCAAGTAGCTGTGGATGGCATGGCTGGTCCCCACAGTAACA	1499
Qy	1304	ACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAG	1363
Db	1500	TCACAGTCATGTTTCCTTGGCTCCAATGATGGGACAGTGCTGAAGGTGCTGACCCAGGTG	1559
Qy	1364	GAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTG	1423
Db	1560	GGCGATCCGG---GGGACCTGAGCCCATCCTCCTGGAAGAGATTGATGCCTACAGCCCTG	1616

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Qy      1424 AAAAATGCAGCTATGATGGAGTCG-----AAGACAAAAGGATCATGGGCATGCAGCTGG 1477
        ||||| | | | | || | ||||| || || |||||
Db      1617 CCCGGTGCAGTGGGAAGCGGACAGCCAAACAGCACGACGGATCATAGGGCTGGAGCTGG 1676

Qy      1478 ACAGAGCAAGCAGCTCTCTGTATGTTGCGTCTCTACCTGTGTGATAAAGGTTCCCCTTG 1537
        ||| | | | | || | || | || | || | || | || | || | || | || | || | || | || |
Db      1677 AACTGAGGGTCACAGGCTTTTTGTGGCTTTTCTGGCTGTATTGTCTACCTCCCTCTCA 1736

Qy      1538 GCCGGTGTGAACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATT 1597
        ||||| || ||||| || | | | |||| | || || || ||||| |
Db      1737 GCCGGTGTGCCCGGCATGGGGCTGTCAGAGGAGCTGTTGGCTTCTCAGGACCCATACT 1796

Qy      1598 GTGGATGG 1605
        |||||
Db      1797 GTGGATGG 1804

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RESULT 10

US-09-254-594-2

; Sequence 2, Application US/09254594

; Patent No. 6566094

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru

; APPLICANT: KIKUCHI, Kaoru

; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y

; FILE REFERENCE: 0020-4527P

; CURRENT APPLICATION NUMBER: US/09/254,594

; CURRENT FILING DATE: 1999-05-11

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 2787

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: Tissue Type: Brain

; NAME/KEY: CDS

; LOCATION: (1)..(2787)

; OTHER INFORMATION: Identification Method: E

; NAME/KEY: misc_feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: Identification Method: P for resulting peptide

US-09-254-594-2

Query Match 12.0%; Score 369.8; DB 4; Length 2787;

Best Local Similarity 55.9%; Pred. No. 7.8e-92;

Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;

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Qy      164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACC 223
        ||||| || |||| | || | |||| | || | | |||| |||| |
Db      176 GGCTGGACTTTCAGAGATTCTGACCTTGAACCGGACCTTGCTTGTGGCTGCCCCGGGATC 235

Qy      224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
        | ||| | | ||| | | | | | | | || ||
Db      236 ACGTTTCTCCTTCGATCTTCAAGCCCAAGAAGAAGGGGAGGGGCTGGTGCCCAACAAGT 295

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Qy 284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
 | | | | | | | | | | | | | | | | | |
 Db 296 T---TCTGACATGGCGGAGCCAAGACATGGAGAATTGTGCTGTCCGGGGAAAGCTGACGG 352

Qy 344 ATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
 | | | | | | | | | | | | | | | | | |
 Db 353 ACGAATGCTACAACCTACATCCGTGTTCTTGTTCCTGGGACTCGCAGACACTCCTTGCCT 412

Qy 404 GTGGAACATAATGCCTTCAACCCCTTCTGCAGAACTATAAGATGGATACATTGGAACCAT 463
 | | | | | | | | | | | | | | | | | |
 Db 413 GTGGAACAAATTCCTTCAGCCCTGTGTGTCGCAGCTATGGGATAACATCTCTGCAACAGG 472

Qy 464 TCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
 | | | | | | | | | | | | | | | | | |
 Db 473 AGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCCTTTGATGCCACCCAGTCCACTGTGG 532

Qy 524 CACTGTTTGCAGATGGAAACTATACTCAGCCACAGTGAAGTGAAGTTCCTTGCCATTGACG 583
 | | | | | | | | | | | | | | | | | |
 Db 533 CCATCTCTGCAGAGGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCAGGCCAGTGATG 592

Qy 584 CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAA 643
 | | | | | | | | | | | | | | | | | |
 Db 593 CTGTGGTTTACAGAAGCCTTGGACCTCAGCCCCCACTCCGTTCTGCAAAGTATGACTCCA 652

Qy 644 AATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCT 703
 | | | | | | | | | | | | | | | | | |
 Db 653 AGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATGTCTACTTCT 712

Qy 704 TCTTCAGGGAAATAGCAGTGGAGTATA---ACACCATGGGAAAGGTAGTTTTCCCAAGAG 760
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 Db 713 TTCTTCCGGAGAAGTCTCTGTGGAGGACGCCCCGGCTGGGGAGGGTGCAGTTTTCCCGGG 772

Qy 761 TGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGA 820
 | | | | | | | | | | | | | | | | | |
 Db 773 TGGCCCGGTGTGTAAACGTGACATGGGTGGCTCACCACGGGCCTTGGATCGCCACTGGA 832

Qy 821 CGTCGTTCTGAAGGCGCGCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
 | | | | | | | | | | | | | | | | | |
 Db 833 CATCCTTCCTTAAGCTGAGGCTCAACTGCTCCGTCCCTGGGGACTCTACCTTCTACTTTG 892

Qy 881 ACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCTCTGGCAA 940
 | | | | | | | | | | | | | | | | | |
 Db 893 ATGTCTTACAGTCCTTAAGTGGGCTGTGAACCTGCATGGGCGCTCTGCCCTCTTTGGGG 952

Qy 941 CGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTG 1000
 | | | | | | | | | | | | | | | | | |
 Db 953 TCTTCACTACTCAGACCAATAGCATTCCTGGGTCTGCAGTCTGCGCCTTCTACCTAGATG 1012

Qy 1001 ACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGA 1060
 | | | | | | | | | | | | | | | | | |
 Db 1013 ACATTGAACGTGGCTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGGATGGGGCCTGGA 1072

Qy 1061 CACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCT 1120
 | | | | | | | | | | | | | | | | | |
 Db 1073 CTCCTGTGTCTGAGGACAAAGTCCCCTCAGGAGGCCAGGTCCTGTGCAGGTGTGGGTG 1132

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Qy      1121 CCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGA 1180
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1133 CAGCTGCCTTATTCTCCTCCTCTCAAGACCTGCCTGACGATGTCCTGCTCTTCATCAAGG 1192

Qy      1181 CGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAA 1240
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1193 CACACCCACTGCTGGATCCCGCTGTGCCACC---TGCCACCCATCAACCTCTCCTCACTC 1249

Qy      1241 CAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGA 1300
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1250 TGACTAGCAGGGCTCTACTGACCCAGGTAGCTGTGGATGGTATGGCTGGCCCCCAGAGAA 1309

Qy      1301 ATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAA 1360
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1310 ATACTACAGTCCTGTTTCTTGGCTCCAATGATGGGACAGTGCTGAAGGTGCTACCTCCAG 1369

Qy      1361 TAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACT 1420
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1370 GGGGACA---GTCTCTGGGACCCGAGCCTATCATATTGGAAGAGATTGATGCCTACAGCC 1426

Qy      1421 CTGAAAAATGCAGCTATGATGG-----AGTCGAAGACAAAAGGATCATGGGCATGCAGC 1474
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1427 ATGCCCCGCTGCAGTGGGAAGCGGTCACCCCGAGCTGCTCGACGGATCATAGGGCTGGAGC 1486

Qy      1475 TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC 1534
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1487 TGGACACTGAGGGTCACAGGCTTTTTGTGGCCTTTTCCTGGATGCATCGTCTACCTCTCTC 1546

Qy      1535 TTGGCCGGTGTGAACGACATGGGAAGTGTAaaaaaacctgtattgcctccagagacccat 1594
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1547 TCAGCCGCTGTGCCCCGGCATGGAGCATGTCAGAGGAGCTGCCTGGCTTCTCTGGACCCAT 1606

Qy      1595 ATTGTGGATGG 1605
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Db      1607 ACTGTGGATGG 1617

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RESULT 11

US-09-254-594-1

; Sequence 1, Application US/09254594

; Patent No. 6566094

; GENERAL INFORMATION:

; APPLICANT: KIMURA, Toru

; APPLICANT: KIKUCHI, Kaoru

; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y

; FILE REFERENCE: 0020-4527P

; CURRENT APPLICATION NUMBER: US/09/254,594

; CURRENT FILING DATE: 1999-05-11

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3195

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: ()..()

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; OTHER INFORMATION: Tissue Type: Brain
; NAME/KEY: 5'UTR
; LOCATION: (1)..(50)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc_feature
; LOCATION: (51)..(2837)
; OTHER INFORMATION: CDS; Identification Method: E
; NAME/KEY: 3'UTR
; LOCATION: (2838)..(3195)
; OTHER INFORMATION: Identification Method: E
US-09-254-594-1
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Query Match          12.0%; Score 369.8; DB 4; Length 3195;
Best Local Similarity 55.9%; Pred. No. 8.5e-92;
Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;
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Qy      164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACC 223
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      226 GGCTGGACTTTTCAGAGATTCTTGACCTTGAACCGGACCTTGCTTGTGGCTGCCCGGGATC 285

Qy      224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      286 ACGTTTTCTCCTTCGATCTTCAAGCCCAAGAAGAAGGGGAGGGGCTGGTGCCCAACAAGT 345

Qy      284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      346 T---TCTGACATGGCGGAGCCAAGACATGGAGAATTGTGCTGTCCGGGGAAAGCTGACGG 402

Qy      344 ATGAGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      403 ACGAATGCTACAACACTACATCCGTGTTCTTGTTCCTGGGACTCGCAGACACTCCTTGCCT 462

Qy      404 GTGGAACATAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCAT 463
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      463 GTGGAACAAATTCCCTTCAGCCCTGTGTGTCGCAGCTATGGGATAACATCTCTGCAACAGG 522

Qy      464 TCGGGGATGAATTTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      523 AGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCCTTTGATGCCACCCAGTCCACTGTGG 582

Qy      524 CACTGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACG 583
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      583 CCATCTCTGCAGAGGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCAGGCCAGTGATG 642

Qy      584 CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAA 643
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      643 CTGTGGTTTACAGAAGCCTTGGACCTCAGCCCCACTCCGTTCTGCAAAGTATGACTCCA 702

Qy      644 AATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCT 703
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Db      703 AGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATGTCTACTTCT 762

Qy      704 TCTTCAGGGAAATAGCAGTGGAGTATA--ACACCATGGGAAAGGTAGTTTCCCAAGAG 760
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Db      763 TTCTTCCGGAGAAGTCTCTGTGGAGGACGCCCGGCCTGGGGAGGGTGCAGTTTCCCGGG 822

Qy      761 TGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGA 820
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Db 823 TGGCCCGGTGTGTAAACGTGACATGGGTGGCTCACCACGGGCCTTGGATCGCCACTGGA 882
 Qy 821 CGTCGTTCCCTGAAGGCGCGCTTGAAGTCTGCTCAGTTCCTGGAGACTCTCATTTTTATTTC 880
 Db 883 CATCCTTCCTTAAGCTGAGGCTCAACTGCTCCGTCCCTGGGGACTCTACCTTCTACTTTG 942
 Qy 881 ACATTCTCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAA 940
 Db 943 ATGTCTTACAGTCCTTAAGTGGGCCTGTGAACCTGCATGGGCGCTCTGCCCTCTTTGGGG 1002
 Qy 941 CGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTG 1000
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 Qy 1001 ACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGA 1060
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 Qy 1061 CACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCT 1120
 Db 1123 CTCCTGTGTCTGAGGACAAAGTCCCCTACCCAGGCCAGGGTCTGTGCAGGTGTGGGTG 1182
 Qy 1121 CCTTAGAAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAAGTTCATCAAGA 1180
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 Qy 1475 TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC 1534
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 Qy 1535 TTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAACCTGTATTGCCTCCAGAGACCCAT 1594
 Db 1597 TCAGCCGCTGTGCCCCGCATGGAGCATGTCAGAGGAGCTGCCTGGCTTCTCTGGACCCAT 1656
 Qy 1595 ATTGTGGATGG 1605
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Db 1657 ACTGTGGATGG 1667

RESULT 12

US-09-833-381-112

; Sequence 112, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 112

; LENGTH: 591

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(591)

; OTHER INFORMATION: n = A,T,C or G

US-09-833-381-112

Query Match 11.9%; Score 368; DB 4; Length 591;

Best Local Similarity 90.2%; Pred. No. 1e-91;

Matches 415; Conservative 0; Mismatches 42; Indels 3; Gaps 2;

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Qy      1952 TGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCT 2011
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Qy      2072 TCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGG 2131
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Qy      2132 ACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCA 2191
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Qy	584	CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCCTGCGGACCGTCAAGCACGATTCAA	643
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Qy	644	AATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCT	703
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Qy	704	TCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGG	763
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Qy	764	CTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCT--GGAGAAACAGTGGAC	821
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Qy	822	GTCGTTCTTGAAGGCGCGCTTGAAGTGCCTCAGTTCCTGGAGACTCTCATTTTTATTTC	881
Db	1088	ATCCTTCTTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCTATTTTGA	1147
Qy	882	CATTCTCCAGGCAGTTACAGATGTGATTCTGATCAACGGGCGTGATGTTGTCCTGGCAAC	941
Db	1148	TGTTTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCTTTGGGGT	1207
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; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-3

Query Match 7.1%; Score 220; DB 4; Length 775;
Best Local Similarity 100.0%; Pred. No. 9.8e-51;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15

US-08-121-713D-57

; Sequence 57, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713D

; FILING DATE: 13-SEP-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 451..2640
US-08-121-713D-57

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Query Match          5.4%; Score 166; DB 1; Length 2854;
Best Local Similarity 53.0%; Pred. No. 1.8e-35;
Matches 532; Conservative 0; Mismatches 415; Indels 57; Gaps 6;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
10493.560 Million cell updates/sec

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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

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2	3038	98.2	3498	10	US-09-957-187-3	Sequence 3, Appli
3	3038	98.2	3498	12	US-10-403-676-31	Sequence 31, Appl
4	3038	98.2	3498	15	US-10-449-548-31	Sequence 31, Appl
5	3037.6	98.2	3055	12	US-10-403-676-27	Sequence 27, Appl
6	3037.6	98.2	3055	15	US-10-449-548-27	Sequence 27, Appl
7	3032	98.0	4250	14	US-10-393-892-30	Sequence 30, Appl
8	3032	98.0	4250	14	US-10-394-382-30	Sequence 30, Appl
9	3032	98.0	4280	15	US-10-120-988-330	Sequence 330, App
10	3030.4	98.0	4250	10	US-09-957-187-84	Sequence 84, Appl
11	3030.4	98.0	4250	12	US-10-403-676-13	Sequence 13, Appl
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15	2975	96.2	3106	12	US-10-403-676-17	Sequence 17, Appl
16	2975	96.2	3106	15	US-10-449-548-17	Sequence 17, Appl
17	2860.8	92.5	2995	12	US-10-403-676-19	Sequence 19, Appl
18	2860.8	92.5	2995	15	US-10-449-548-19	Sequence 19, Appl
19	2746.8	88.8	2944	12	US-10-403-676-29	Sequence 29, Appl
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21	2727.4	88.2	3983	12	US-10-403-676-45	Sequence 45, Appl
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39	1788.6	57.8	1921	15	US-10-449-548-15	Sequence 15, Appl
40	1719.4	55.6	1908	12	US-10-403-676-35	Sequence 35, Appl
41	1719.4	55.6	1908	15	US-10-449-548-35	Sequence 35, Appl
42	1476.2	47.7	1492	12	US-10-403-676-23	Sequence 23, Appl
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44	1422.2	46.0	1438	12	US-10-403-676-25	Sequence 25, Appl
45	1422.2	46.0	1438	15	US-10-449-548-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
 US-09-991-053-3
 ; Sequence 3, Application US/09991053
 ; Publication No. US20030003532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shimkets, Richard A.

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; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
; TITLE OF INVENTION: MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 15966-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991,053
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(3030)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3047)
; OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-3
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Query Match          98.2%; Score 3038; DB 10; Length 3498;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;
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Qy      241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
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Db	814	 CTTGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	873
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	874	 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	933
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAT	780
Db	934	 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAT	993
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	840
Db	994	 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	1053
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1054	 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1113
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1114	 GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1173
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1174	 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	 GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	 TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1413
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCCTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320

Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1593
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1953
Qy	1741	TCCCTCTTGCCAGCACAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1954	TCCCTCTTGCCAGCACAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	2013
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2014	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2073
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAA	1920
Db	2074	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAA	2133
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2134	GGCCACGACCAGCTGGTTCCCGTCACCTCTTGCCATTGCAGTCATCCTGGCTTTCGTC	2193
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2194	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2253
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2254	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2313
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2314	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2373

Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2374	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2433
Qy	2221	ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2280
Db	2434	ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2493
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2494	ACCCCAACGCTGCAGCAGAAGCGGGAACCCAGCCGCGGCACCCGCGAGTGGGAGAGGAAC	2553
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2554	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2613
Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCCATC	2460
Db	2614	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCCATC	2673
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2520
Db	2674	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAG	2733
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2734	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2793
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC AAA	2640
Db	2794	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCC AAA	2853
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2854	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2913
Qy	2701	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2914	AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2973
Qy	2761	CCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAGAAACAACACTAA	2819
Db	2974	CCCACGAACCTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	3033
Qy	2820	CTCCTCCAATTCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC	2878
Db	3034	CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC	3093
Qy	2879	CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2938
Db	3094	CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	3153
Qy	2939	CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	2998
Db	3154	CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	3213

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Qy      2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
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Db      3214 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3273

Qy      3059 CCACATCCATGAAGCCCAATGATGCGGTACATAA 3093
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Db      3274 CCACATCCATGAAGCCCAATGATGCGGTACATAA 3308

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RESULT 2

US-09-957-187-3

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; Sequence 3, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: LaRoche, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957,187
; CURRENT FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(3030)
; NAME/KEY: misc_feature
; LOCATION: (3047)
; OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-957-187-3

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Query Match          98.2%; Score 3038; DB 10; Length 3498;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db      214 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
          |||
Db      274 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy      121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180

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Db	334	 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	393
Qy	181	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	394	 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	453
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	454	 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	513
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	360
Db	514	 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	573
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	574	 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	633
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	634	 AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	693
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	694	 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	753
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	754	 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	813
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	814	 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	873
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	874	 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	933
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	934	 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	993
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAAGGCGCGC	840
Db	994	 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAAGGCGCGC	1053
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1054	 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1113
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1114	 GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1173
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTCTTTACT	1020

Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTCTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	TCCAATGAGTTCCCTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1413
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1593
Qy	1381	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1953
Qy	1741	TCCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1954	TCCCTCTTGCCCAGCACAAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	2013
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCCTTGGGG	1860
Db	2014	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCCTTGGGG	2073

Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAA	1920
Db	2074	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAA	2133
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2134	GGCCACGACCAGCTGGTTCCCGTCACCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	2193
Qy	1981	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2194	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2253
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2254	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2313
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2314	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2373
Qy	2161	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2374	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2433
Qy	2221	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2280
Db	2434	ATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCA	2493
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2494	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCACCCGCGAGTGGGAGAGGAAC	2553
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2554	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2613
Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2460
Db	2614	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2673
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2520
Db	2674	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2733
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2734	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2793
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2794	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2853
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2854	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2913

Qy 2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
 |||
 Db 2914 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2973
 |||
 Qy 2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA 2819
 |||
 Db 2974 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA 3033
 |||
 Qy 2820 CTCCTCCAATTCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC 2878
 |||
 Db 3034 CCCCACAATTCTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC 3093
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 Qy 2879 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGCCAGG 2938
 |||
 Db 3094 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGCCAGG 3153
 |||
 Qy 2939 CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC 2998
 |||
 Db 3154 CCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC 3213
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 Qy 2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCTTT 3058
 |||
 Db 3214 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCTTT 3273
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 Qy 3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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 Db 3274 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3308
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RESULT 3

US-10-403-676-31

; Sequence 31, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: LaRochelle, William J.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Li, Li
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Reiger, Daniel


```

; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 31
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(3030)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3047)..(3047)
; OTHER INFORMATION: Wherein n may be a, c, g or t
US-10-403-676-31

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Query Match          98.2%;  Score 3038;  DB 12;  Length 3498;
Best Local Similarity 99.3%;  Pred. No. 0;
Matches 3072;  Conservative 0;  Mismatches 21;  Indels 2;  Gaps 2;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db          214 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 273
             |||
Qy          61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Db 274 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy 121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
|||||

Db 334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy 181 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
|||||

Db 394 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy 241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
|||||

Db 454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 513

Qy 301 CAGGCCGATGTAGACACATGCAGAATGAAGGAAAACATAAGGATGAGTGCCACAACCTTT 360
|||||

Db 514 CAGGCCGATGTAGACACATGCAGAATGAAGGAAAACATAAGGATGAGTGCCACAACCTTT 573

Qy 361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 420
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Db 574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 633

Qy 421 AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Db 634 AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy 481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Db 694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy 541 AAACCTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
|||||

Db 754 AAACCTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy 601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Db 814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873

Qy 661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAAATAGCA 720
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Db 874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAAATAGCA 933

Qy 721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
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Db 934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy 781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC 840
|||||

Db 994 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC 1053

Qy 841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
|||||

Db 1054 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1113

Qy 901 GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
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Db 1114 GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1173

Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGT'TTTTACT	1020
Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGT'TTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCTGATGATACCTGAACCTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	TCCAATGAGTTCCTGATGATACCTGAACCTTCATCAAGACGCACCCGCTCATGGATGAG	1413
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGT'TTTTCTG	1320
Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGT'TTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGT'TTTTGGCCAGAATAGGAAATAGTGGT'TTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGT'TTTTGGCCAGAATAGGAAATAGTGGT'TTTTCTA	1593
Qy	1381	AATGACAGCCT'TTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCT'TTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1953
Qy	1741	TCCCTCTTGCCAGCACAACCACATCAGATTTCGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1954	TCCCTCTTGCCAGCACAACCACATCAGATTTCGACGGCTCAAGAGGGGTATGAGTCTAGG	2013

Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2014	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2073
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAA	1920
Db	2074	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAA	2133
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2134	GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	2193
Qy	1981	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2194	ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2253
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100
Db	2254	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2313
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2314	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2373
Qy	2161	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2374	GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2433
Qy	2221	ATGCTCATTAAGCAGACCAGCACACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2280
Db	2434	ATGCTCATTAAGCAGACCAGCACACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2493
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2494	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2553
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2554	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2613
Qy	2401	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2460
Db	2614	ACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATC	2673
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2520
Db	2674	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAATGAGCGAGGTGGCCCAG	2733
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2734	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2793
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2640
Db	2794	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAA	2853
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700

Db	2854		GTTCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2913
Qy	2701		AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2914		AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2973
Qy	2761		CCACGAACTCGCTCAGAGAAGCCACCAGGCCACC-ACTCTCAAAGAAACAACACTAA	2819
Db	2974		CCACGAACTCGCTCAGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	3033
Qy	2820		CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC	2878
Db	3034		CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC	3093
Qy	2879		CGCCCCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	2938
Db	3094		CGCCCCCGCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG	3153
Qy	2939		CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	2998
Db	3154		CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGC	3213
Qy	2999		TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT	3058
Db	3214		TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT	3273
Qy	3059		CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3093
Db	3274		CCACATCCATGAAGCCCAATGATGCGTGTACATAA	3308

RESULT 4

US-10-449-548-31

; Sequence 31, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

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; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 31
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(3030)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3047)..(3047)
; OTHER INFORMATION: Wherein n may be a, c, g or t
US-10-449-548-31

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Query Match          98.2%; Score 3038; DB 15; Length 3498;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
        |||
Db      214 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
        |||
Db      274 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy      121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
        |||
Db      334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy      181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
        |||
Db      394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy      241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
        |||
Db      454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 513

Qy      301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 360
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Db      514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 573

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Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	574	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	633
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	634	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	693
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	694	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	753
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	754	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	813
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	814	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	873
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	874	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	933
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	934	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	993
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	840
Db	994	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	1053
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1054	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1113
Qy	901	GATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1114	GATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1173
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1174	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1233
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1234	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1293
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1294	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1353
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1354	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1413

Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1414	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1473
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1474	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1533
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1534	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1593
Qy	1381	AATGACAGCCTTTTCTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1594	AATGACAGCCTTTTCTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1653
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1654	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1713
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1714	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1773
Qy	1561	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1774	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1833
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1834	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1893
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1740
Db	1894	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT	1953
Qy	1741	TCCCTCTTGCCCAGCACAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	1800
Db	1954	TCCCTCTTGCCCAGCACAACCACATCAGATTGACGGCTCAAGAGGGGTATGAGTCTAGG	2013
Qy	1801	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	1860
Db	2014	GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG	2073
Qy	1861	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAA	1920
Db	2074	GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAA	2133
Qy	1921	GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	1980
Db	2134	GGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC	2193
Qy	1981	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2040
Db	2194	ATGGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC	2253
Qy	2041	GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC	2100

Db	2254	 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTACCCACTCGCGCCGGGGCTCCATGAGC	2313
Qy	2101	AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2160
Db	2314	 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG	2373
Qy	2161	GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2220
Db	2374	 GCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG	2433
Qy	2221	ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2280
Db	2434	 ATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA	2493
Qy	2281	ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2340
Db	2494	 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC	2553
Qy	2341	CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2400
Db	2554	 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCC	2613
Qy	2401	ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	2460
Db	2614	 ACGGACCTGCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC	2673
Qy	2461	ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCAG	2520
Db	2674	 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCAG	2733
Qy	2521	ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2580
Db	2734	 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC	2793
Qy	2581	AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAA	2640
Db	2794	 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAA	2853
Qy	2641	GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2854	 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA	2913
Qy	2701	AGCAAGCGGTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2760
Db	2914	 AGCAAGCGGTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC	2973
Qy	2761	CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAGAAACAACACTAA	2819
Db	2974	 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA	3033
Qy	2820	CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC	2878
Db	3034	 CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC	3093
Qy	2879	CGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCATCTGGCCAGG	2938

Db 3094 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 3153
 Qy 2939 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGC 2998
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 Db 3154 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGC 3213
 Qy 2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCTTTGCTCCCCTTT 3058
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 3214 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCTTTGCTCCCCTTT 3273
 Qy 3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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 Db 3274 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3308

RESULT 5

US-10-403-676-27

; Sequence 27, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John

; APPLICANT: Anderson, David W.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Burgess, Catherine E.

; APPLICANT: Casman, Stacie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Grosse, William M.

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen

; APPLICANT: LaRochelle, William J.

; APPLICANT: Lepley, Denise M.

; APPLICANT: Li, Li

; APPLICANT: Liu, Xiaohong

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Peyman, John A.

; APPLICANT: Rastelli, Luca

; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Taupier, Raymond J.

; APPLICANT: Vernet, Corine

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

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; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 27
;   LENGTH: 3055
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(3055)
US-10-403-676-27

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Query Match          98.2%;   Score 3037.6;   DB 12;   Length 3055;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 3040;   Conservative    0;   Mismatches    4;   Indels    0;   Gaps    0;

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Qy      47 CTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAA 106
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Db      3  CCGGATCCGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAA 62

Qy     107 AACAGTATCCGGTGTTTGTGGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC 166
      |||||
Db     63  AACAGTATCCGGTGTTTGTGGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC 122

Qy     167 TGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATA 226
      |||||
Db     123 TGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATA 182

Qy     227 TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGA 286
      |||||
Db     183 TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGA 242

Qy     287 CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG 346
      |||||
Db     243 CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG 302

Qy     347 AGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTG 406
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Db     303 AGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTG 362

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Qy	407	GAAC TAATGCCTTCAACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCG	466
Db	363	GAAC TAATGCCTTCAACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCG	422
Qy	467	GGGATGAATT CAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC	526
Db	423	GGGATGAATT CAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC	482
Qy	527	TGTTTGCAGATGGAAAAC TATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG	586
Db	483	TGTTTGCAGATGGAAAAC TATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG	542
Qy	587	TCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAT	646
Db	543	TCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAT	602
Qy	647	GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT	706
Db	603	GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT	662
Qy	707	TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC	766
Db	663	TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC	722
Qy	767	AGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGT	826
Db	723	AGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGT	782
Qy	827	TCCTGAAGGCGCGCTTGAAC TGCTCAGTTCCTGGAGACTCTCATTTTTATTTC AACATT C	886
Db	783	TCCTGAAGGCGCGCTTGAAC TGCTCAGTTCCTGGAGACTCTCATTTTTATTTC AACATT C	842
Qy	887	TCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTT	946
Db	843	TCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTT	902
Qy	947	CTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTG	1006
Db	903	CTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTG	962
Qy	1007	CCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAG	1066
Db	963	CCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAG	1022
Qy	1067	TTCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAG	1126
Db	1023	TTCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAG	1082
Qy	1127	AAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACC	1186
Db	1083	AAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACC	1142
Qy	1187	CGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGG	1246
Db	1143	CGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGG	1202
Qy	1247	TCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACA	1306

Db	1203	 TCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACA	1262
Qy	1307	CTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAA	1366
Db	1263	 CTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAA	1322
Qy	1367	ATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAA	1426
Db	1323	 ATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAA	1382
Qy	1427	AATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAA	1486
Db	1383	 AATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAA	1442
Qy	1487	GCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTG	1546
Db	1443	 GCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTG	1502
Qy	1547	AACGACATGGGAAGTGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGA	1606
Db	1503	 AACGACATGGGAAGTGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGA	1562
Qy	1607	TAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGG	1666
Db	1563	 TAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGG	1622
Qy	1667	ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA	1726
Db	1623	 ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA	1682
Qy	1727	ATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGG	1786
Db	1683	 ATGGGCATTCCAGTTCCTCTTGCCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGG	1742
Qy	1787	GGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCA	1846
Db	1743	 GGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCA	1802
Qy	1847	CAGACCCTTTGGGGGAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGG	1906
Db	1803	 CAGACCCTTTGGGGGAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGG	1862
Qy	1907	AAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCA	1966
Db	1863	 AAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCA	1922
Qy	1967	TCCTGGCTTTTCGTTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATC	2026
Db	1923	 TCCTGGCTTTTCGTTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATC	1982
Qy	2027	ATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCC	2086
Db	1983	 ATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCC	2042
Qy	2087	GGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAG	2146

Db 2043 GGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAG 2102

Qy 2147 ACCCAAAGCCGGAGGCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCG 2206
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Db 2103 ACCCAAAGCCGGAGGCCATCCTCAGCCACTCATGCACAACGGCAAGCTCGCCACTCCCG 2162

Qy 2207 GCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCC 2266
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Db 2163 GCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCC 2222

Qy 2267 CCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCG 2326
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Db 2223 CCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCG 2282

Qy 2327 AGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCT 2386
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Db 2283 AGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCT 2342

Qy 2387 CCCCTGTGATTCCACGGACCTGCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGG 2446
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Db 2343 CCCCTGTGATTCCACGGACCTGCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGG 2402

Qy 2447 TGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGA 2506
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Db 2403 TGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGA 2462

Qy 2507 GCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCA 2566
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Db 2463 GCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCA 2522

Qy 2567 AGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACA 2626
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Db 2523 AGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACA 2582

Qy 2627 GCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGT 2686
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Db 2583 GCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGT 2642

Qy 2687 CTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACT 2746
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Db 2643 CTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACT 2702

Qy 2747 ATAAGAGGAGCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAA 2806
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Db 2703 ATAAGAGGAGCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAA 2762

Qy 2807 GAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2866
 |||

Db 2763 GAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2822

Qy 2867 GAGACAACCCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2926
 |||

Db 2823 GAGACAACCCGCCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2882

Qy 2927 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGA 2986
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Db 2883 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGA 2942

Qy 2987 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCT 3046
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 Db 2943 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCT 3002
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 Db 3003 TTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3046

RESULT 6

US-10-449-548-27

; Sequence 27, Application US/10449548
 ; Publication No. US20040018977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alvarez, Enrique
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Dhanabal, Mohanraj
 ; APPLICANT: Khramtsov, Nikolai V.
 ; APPLICANT: LaRochelle, William J.
 ; APPLICANT: Li, Li
 ; APPLICANT: Lichenstein, Henri
 ; APPLICANT: Ooi, Chean Eng
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Zhong, Mei
 ; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
 ; FILE REFERENCE: 15966-540CIP2
 ; CURRENT APPLICATION NUMBER: US/10/449,548
 ; CURRENT FILING DATE: 2003-05-30
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/123,667
 ; PRIOR FILING DATE: 1999-03-09
 ; PRIOR APPLICATION NUMBER: 60/234,082
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: 60/233,798
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 60/174,485
 ; PRIOR FILING DATE: 2000-01-04
 ; PRIOR APPLICATION NUMBER: 10/403,676
 ; PRIOR FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: 60/371,002
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/384,798
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/402,407
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 60/443,062
 ; PRIOR FILING DATE: 2003-01-28
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: CuraSeqList version 0.1
 ; SEQ ID NO 27
 ; LENGTH: 3055
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

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;   NAME/KEY: CDS
;   LOCATION: (2)..(3055)
US-10-449-548-27

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Query Match 98.2%; Score 3037.6; DB 15; Length 3055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3040; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	47	CTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAA	106
Db	3	CCGGATCCGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAA	62
Qy	107	AACAGTATCCGGTGTGTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC	166
Db	63	AACAGTATCCGGTGTGTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC	122
Qy	167	TGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATA	226
Db	123	TGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATA	182
Qy	227	TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGA	286
Db	183	TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGA	242
Qy	287	CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG	346
Db	243	CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG	302
Qy	347	AGTGCCACAAC TTTATTAAAGTTCTTCTAAAGAAAACGATGATGCATTGTTTGTCTGTG	406
Db	303	AGTGCCACAAC TTTATTAAAGTTCTTCTAAAGAAAACGATGATGCATTGTTTGTCTGTG	362
Qy	407	GAAC TAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCTG	466
Db	363	GAAC TAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCTG	422
Qy	467	GGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC	526
Db	423	GGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC	482
Qy	527	TGTTTGCAGATGGAAAAC TATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG	586
Db	483	TGTTTGCAGATGGAAAAC TATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG	542
Qy	587	TCATTTACCGGAGTCTTGAGAAAGCCCTACCTGCGGACCGTCAAGCACGATTCAAAT	646
Db	543	TCATTTACCGGAGTCTTGAGAAAGCCCTACCTGCGGACCGTCAAGCACGATTCAAAT	602
Qy	647	GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT	706
Db	603	GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT	662
Qy	707	TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC	766
Db	663	TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC	722
Qy	767	AGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGT	826

Db	723		AGGTTTGTAAAGATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGT	782
Qy	827		TCCTGAAGGCGCGCTTGAAC'TGCTCAGTTCCTGGAGACTCTCATT'TTTATTTCAACATTC	886
Db	783		TCCTGAAGGCGCGCTTGAAC'TGCTCAGTTCCTGGAGACTCTCATT'TTTATTTCAACATTC	842
Qy	887		TCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTT	946
Db	843		TCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTT	902
Qy	947		CTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTG	1006
Db	903		CTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTG	962
Qy	1007		CCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAG	1066
Db	963		CCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAG	1022
Qy	1067		TTCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAG	1126
Db	1023		TTCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAG	1082
Qy	1127		AAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAAC'TTCATCAAGACGCACC	1186
Db	1083		AAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAAC'TTCATCAAGACGCACC	1142
Qy	1187		CGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGG	1246
Db	1143		CGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGG	1202
Qy	1247		TCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACA	1306
Db	1203		TCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACA	1262
Qy	1307		CTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAA	1366
Db	1263		CTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAA	1322
Qy	1367		ATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAAC'TCTGAAA	1426
Db	1323		ATAGTGGTTTTCTAAATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAAC'TCTGAAA	1382
Qy	1427		AATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAA	1486
Db	1383		AATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAA	1442
Qy	1487		GCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTG	1546
Db	1443		GCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTG	1502
Qy	1547		AACGACATGGGAAGTGTAaaaaaacctgtattgcctccagagaccCATATTGTGGATGGA	1606
Db	1503		AACGACATGGGAAGTGTAaaaaaacctgtattgcctccagagaccCATATTGTGGATGGA	1562
Qy	1607		TAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGGAGCAGG	1666

Db	1563	TAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGTAGCAGG	1622
Qy	1667	ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA	1726
Db	1623	ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA	1682
Qy	1727	ATGGGCATTCCAGTTCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGG	1786
Db	1683	ATGGGCATTCCAGTTCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGG	1742
Qy	1787	GGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCA	1846
Db	1743	GGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCA	1802
Qy	1847	CAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGG	1906
Db	1803	CAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGG	1862
Qy	1907	AAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCA	1966
Db	1863	AAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCA	1922
Qy	1967	TCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATC	2026
Db	1923	TCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATC	1982
Qy	2027	ATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCC	2086
Db	1983	ATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCC	2042
Qy	2087	GGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAG	2146
Db	2043	GGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAG	2102
Qy	2147	ACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCG	2206
Db	2103	ACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCG	2162
Qy	2207	GCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCC	2266
Db	2163	GCAACACGGCCAAGATGCTCATTAAGCAGACCAGCACCTGGACCTGACGGCCCTCC	2222
Qy	2267	CCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCG	2326
Db	2223	CCACCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCAGCCGCGGCAGCCGCG	2282
Qy	2327	AGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCT	2386
Db	2283	AGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCT	2342
Qy	2387	CCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCTCCCCAGCCACATCCCAGCGTGG	2446
Db	2343	CCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCTCCCCAGCCACATCCCAGCGTGG	2402
Qy	2447	TGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGA	2506
Db	2403	TGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCAAAATGA	2462

Qy 2507 GCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCA 2566
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 Db 2463 GCGAGGTGGCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCA 2522

 Qy 2567 AGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACA 2626
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2523 AGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACA 2582

 Qy 2627 GCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGT 2686
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2583 GCCTGCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGT 2642

 Qy 2687 CTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACT 2746
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2643 CTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACT 2702

 Qy 2747 ATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAA 2806
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2703 ATAAGAGGAGCTACCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAA 2762

 Qy 2807 GAAACAACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2866
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2763 GAAACAACACTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2822

 Qy 2867 GAGACAACCCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2926
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2823 GAGACAACCCGCCGCCCGCCCCGAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2882

 Qy 2927 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGA 2986
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2883 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTACTGA 2942

 Qy 2987 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCT 3046
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2943 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCT 3002

 Qy 3047 TTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3090
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 Db 3003 TTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3046

RESULT 7

US-10-393-892-30

; Sequence 30, Application US/10393892

; Publication No. US20030186302A1

; GENERAL INFORMATION:

; APPLICANT: WANG, YIXIN

; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS

; FILE REFERENCE: CDS 267 US NP

; CURRENT APPLICATION NUMBER: US/10/393,892

; CURRENT FILING DATE: 2003-03-21

; PRIOR APPLICATION NUMBER: 60/368,798

; PRIOR FILING DATE: 2002-03-29

; NUMBER OF SEQ ID NOS: 49

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 4250
; TYPE: DNA
; ORGANISM: human
US-10-393-892-30

Query Match 98.0%; Score 3032; DB 14; Length 4250;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db     250 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy     61 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG 369

Qy    121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy    181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 489

Qy    241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 549

Qy    301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTT 609

Qy    361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 669

Qy    421 AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 729

Qy    481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 789

Qy    541 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 849

Qy    601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 909

Qy    661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 969
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Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAAT	780
Db	970	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAAT	1029
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	840
Db	1030	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	1089
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1090	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1149
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1150	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1209
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1210	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1269
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1270	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1329
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1330	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1389
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1390	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1449
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1450	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1509
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1510	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1569
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1570	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1629
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1630	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1689
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1690	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1749
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1750	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1809
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620

Db	1810	 TGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1869
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1870	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1929
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1930	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1989
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	1990	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	2049
Qy	1750	CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	2050	CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2109
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	2110	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	2169
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2170	TCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGAC	2229
Qy	1930	CAGCTGGTTCCCGTCACCCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	2230	CAGCTGGTTCCCGTCACCCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2289
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2290	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2349
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2350	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2409
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2410	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2469
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2470	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2529
Qy	2230	AAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289
Db	2530	AAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2589
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2590	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2649
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2409

Db 2650 ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2709

Qy 2410 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2469
 |||

Db 2710 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2769

Qy 2470 GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG 2529
 |||

Db 2770 GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG 2829

Qy 2530 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2589
 |||

Db 2830 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2889

Qy 2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG 2649
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Db 2890 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG 2949

Qy 2650 CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
 |||

Db 2950 CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3009

Qy 2710 CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC 2769
 |||

Db 3010 CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC 3069

Qy 2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
 |||

Db 3070 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 3129

Qy 2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG 2889
 |||

Db 3130 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG 3189

Qy 2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
 |||

Db 3190 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3249

Qy 2950 TCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTGCGGGCTGAAGCGTACG 3009
 |||

Db 3250 TCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTGCGGGCTGAAGCGTACG 3309

Qy 3010 CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
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Db 3310 CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3369

Qy 3070 AAGCCCAATGATGCGTGTACATAA 3093
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Db 3370 AAGCCCAATGATGCGTGTACATAA 3393

RESULT 8

US-10-394-382-30

; Sequence 30, Application US/10394382

; Publication No. US20030186303A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Yixin

; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS
; FILE REFERENCE: CDS 266 US NP
; CURRENT APPLICATION NUMBER: US/10/394,382
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,687
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 4250
; TYPE: DNA
; ORGANISM: human
US-10-394-382-30

Query Match 98.0%; Score 3032; DB 14; Length 4250;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db      250 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      310 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 369

Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db      370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy     181 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db      430 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 489

Qy     241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      490 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 549

Qy     301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAAACATAAGGATGAGTGCCACAACCTT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      550 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAAACATAAGGATGAGTGCCACAACCTT 609

Qy     361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      610 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 669

Qy     421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      670 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 729

Qy     481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Db      730 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 789

Qy     541 AAATACTACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Db      790 AAATACTACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 849
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Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	850	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	909
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	910	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	969
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	970	GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	1029
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	840
Db	1030	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCCTGAAGGCGCGC	1089
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1090	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTATTTCAACATTCTCCAGGCAGTTACA	1149
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1150	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1209
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1210	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1269
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1270	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1329
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1330	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1389
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1390	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1449
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1450	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1509
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1510	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1569
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1570	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1629
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1630	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1689

Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1690	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1749
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1750	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1809
Qy	1561	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1810	TGTAACAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1869
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1870	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1929
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1930	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1989
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	1990	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	2049
Qy	1750	CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	2050	CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2109
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	2110	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	2169
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2170	TCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAAAGGCCACGAC	2229
Qy	1930	CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	2230	CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2289
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2290	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2349
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2350	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2409
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2410	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2469
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2470	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2529
Qy	2230	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289

Db	2530	 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2589
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2590	 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2649
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2409
Db	2650	 ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2709
Qy	2410	CCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2469
Db	2710	 CCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2769
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCAGATGGCGCTG	2529
Db	2770	 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCAGATGGCGCTG	2829
Qy	2530	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2830	 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2889
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	2890	 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2949
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	2950	 CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	3009
Qy	2710	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769
Db	3010	 CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	3069
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	2829
Db	3070	 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	3129
Qy	2830	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	2889
Db	3130	 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	3189
Qy	2890	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	2949
Db	3190	 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	3249
Qy	2950	TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3009
Db	3250	 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3309
Qy	3010	CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG	3069
Db	3310	 CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG	3369
Qy	3070	AAGCCCAATGATGCGTGACATAA	3093

Db 3370 AAGCCCAATGATGCGTGACATAA 3393

RESULT 9

US-10-120-988-330

; Sequence 330, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 330
; LENGTH: 4280
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (267)..(3410)
US-10-120-988-330

Query Match 98.0%; Score 3032; DB 15; Length 4280;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

Qy	1	ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC	60
Db	267	ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC	326
Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	120
Db	327	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	386
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	387	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	446
Qy	181	ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	447	ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	506
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	507	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	566
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAACATAAGGATGAGTGCCACAACCTT	360

Db	567	 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT	626
Qy	361	ATTAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	627	ATTAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	686
Qy	421	AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	687	AACCCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	746
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	747	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	806
Qy	541	AACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	807	AACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	866
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	867	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	926
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	927	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	986
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAT	780
Db	987	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAAGAAT	1046
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	840
Db	1047	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	1106
Qy	841	TTGAACTGCTCAGTTCCTGGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1107	TTGAACTGCTCAGTTCCTGGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1166
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1167	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1226
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1227	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1286
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1287	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1346
Qy	1081	GTTCTTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1347	GTTCTTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1406
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200

Db	1407	TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1466
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1467	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1526
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGT'TTTTCTG	1320
Db	1527	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGT'TTTTCTG	1586
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGT'TTTCTA	1380
Db	1587	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGT'TTTCTA	1646
Qy	1381	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAATGCAGCTATGAT	1440
Db	1647	AATGACAGCCTTTTCTGGAGGAGATGAGTGTTTACAACCTCTGAAAATGCAGCTATGAT	1706
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1707	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1766
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAAGGTTCCCCTTGCCCGGTGTGAACGACATGGGAAG	1560
Db	1767	GTTGCGTTCTCTACCTGTGTGATAAAAGGTTCCCCTTGCCCGGTGTGAACGACATGGGAAG	1826
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1827	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1886
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1887	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1946
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1947	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	2006
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	2007	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	2066
Qy	1750	CCCAGCACACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	2067	CCCAGCACACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2126
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGAGTGTCT	1869
Db	2127	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGAGTGTCT	2186
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2187	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	2246
Qy	1930	CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	2247	CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2306

Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2307	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2366
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2367	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2426
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2427	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2486
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2487	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2546
Qy	2230	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289
Db	2547	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2606
Qy	2290	CTGCAGCAGAAGCGGAAGCCAGCCGCGGAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2607	CTGCAGCAGAAGCGGAAGCCAGCCGCGGAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2666
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2409
Db	2667	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2726
Qy	2410	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCCTGCCCATCACGCAGCAG	2469
Db	2727	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCCTGCCCATCACGCAGCAG	2786
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG	2529
Db	2787	GGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG	2846
Qy	2530	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2847	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2906
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	2907	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2966
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	2967	CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	3026
Qy	2710	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769
Db	3027	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	3086
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT	2829
Db	3087	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT	3146

Qy 2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCGCCG 2889
 |||
 Db 3147 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCGCCG 3206
 Qy 2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
 |||
 Db 3207 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3266
 Qy 2950 TCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGCTGAAGCGTACG 3009
 |||
 Db 3267 TCGAGGCAGCCAGCCTCAACGCCTACAACCTACTGACAAGGTCGGGGCTGAAGCGTACG 3326
 Qy 3010 CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
 |||
 Db 3327 CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3386
 Qy 3070 AAGCCCAATGATGCGTGTACATAA 3093
 |||
 Db 3387 AAGCCCAATGATGCGTGTACATAA 3410

RESULT 10

US-09-957-187-84

; Sequence 84, Application US/09957187
 ; Publication No. US20030054514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: LaRochelle, William
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
 ; FILE REFERENCE: 15966-540 CIP
 ; CURRENT APPLICATION NUMBER: US/09/957,187
 ; CURRENT FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 60/123,667
 ; PRIOR FILING DATE: 1999-03-09
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/234,082
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: 60/233,798
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 60/174,485
 ; PRIOR FILING DATE: 2000-01-04
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 84
 ; LENGTH: 4250
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (250)..(3390)
 US-09-957-187-84

Query Match 98.0%; Score 3030.4; DB 10; Length 4250;
 Best Local Similarity 98.3%; Pred. No. 0;
 Matches 3092; Conservative 0; Mismatches 1; Indels 51; Gaps 1;

Qy	1	ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC	60
Db	250	ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC	309
Qy	61	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG	120
Db	310	CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATTGCAACTATACAAAACAGTATCCGGTG	369
Qy	121	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	180
Db	370	TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG	429
Qy	181	ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	430	ATTATGATCATGAACGGAACCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	489
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	490	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	549
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAAC'TTT	360
Db	550	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAAC'TTT	609
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	610	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	669
Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	670	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	729
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	730	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	789
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	790	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	849
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	660
Db	850	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA	909
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	910	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	969
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	780
Db	970	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	1029
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	840
Db	1030	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCTGAAGGCGCGC	1089
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	900

Db	1090	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTATTTC AACATTCTCCAGGCAGTTACA	1149
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1150	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1209
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1210	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1269
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1270	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1329
Qy	1081	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1140
Db	1330	GTTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC	1389
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1390	TCCAATGAGTTCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1449
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1450	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1509
Qy	1261	ACCAAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1510	ACCAAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1569
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTTCTA	1380
Db	1570	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTTCTA	1629
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1630	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1689
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1690	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1749
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1750	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1809
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1810	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1869
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGCC	1680
Db	1870	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGCC	1929
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726

Db	1930	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1989
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	1990	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	2049
Qy	1750	CCCAGCACACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	2050	CCCAGCACACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2109
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGAGTGTCT	1869
Db	2110	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGAGTGTCT	2169
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2170	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	2229
Qy	1930	CAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTTCGTCATGGGGGCC	1989
Db	2230	CAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTTCGTCATGGGGGCC	2289
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2290	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2349
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2350	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2409
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2410	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2469
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2470	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2529
Qy	2230	AAAGCAGACCAGCACACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289
Db	2530	AAAGCAGACCAGCACACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2589
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2590	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2649
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2409
Db	2650	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2709
Qy	2410	CCCCTGCGGGCCTCCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2469
Db	2710	CCCCTGCGGGCCTCCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2769
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2529
Db	2770	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2829

Qy	2530	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2830	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2889
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	2890	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2949
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	2950	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	3009
Qy	2710	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769
Db	3010	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	3069
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	2829
Db	3070	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	3129
Qy	2830	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	2889
Db	3130	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	3189
Qy	2890	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	2949
Db	3190	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	3249
Qy	2950	TCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3009
Db	3250	TCGAGGCAGCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3309
Qy	3010	CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG	3069
Db	3310	CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG	3369
Qy	3070	AAGCCCAATGATGCGGTGTACATAA	3093
Db	3370	AAGCCCAATGATGCGGTGTACATAA	3393

RESULT 11

US-10-403-676-13

; Sequence 13, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gusev, Vladimir Y.

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; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 13
; LENGTH: 4250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (250)..(3390)
US-10-403-676-13

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Query Match

98.0%; Score 3030.4; DB 12; Length 4250;

Best Local Similarity 98.3%; Pred. No. 0;
Matches 3092; Conservative 0; Mismatches 1; Indels 51; Gaps 1;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC 60
      |||
Db    250 ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
      |||
Db    310 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATTGCAACTATACAAAACAGTATCCGGTG 369

Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
      |||
Db    370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy     181 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
      |||
Db    430 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 489

Qy     241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
      |||
Db    490 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 549

Qy     301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAAACATAAGGATGAGTGCCACAACTTT 360
      |||
Db    550 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAAACATAAGGATGAGTGCCACAACTTT 609

Qy     361 ATTAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 420
      |||
Db    610 ATTAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC 669

Qy     421 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
      |||
Db    670 AACCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 729

Qy     481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
      |||
Db    730 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 789

Qy     541 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
      |||
Db    790 AAATATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 849

Qy     601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
      |||
Db    850 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 909

Qy     661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
      |||
Db    910 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 969

Qy     721 GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
      |||
Db    970 GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1029

Qy     781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC 840
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Db	1030	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	1089
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	1090	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	1149
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1150	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCTGGCAACGTTTTCTACACCTTATAAC	1209
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1210	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1269
Qy	1021	GGGAGATTCAAGGAACAGAACTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1270	GGGAGATTCAAGGAACAGAACTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1329
Qy	1081	GTTCTTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGAACC	1140
Db	1330	GTTCTTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGAACC	1389
Qy	1141	TCCAATGAGTTCCTTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1390	TCCAATGAGTTCCTTGATGATACCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1449
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCTTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1450	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCTTGAGAACAATGGTCAGATACCGCCTT	1509
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1510	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1569
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1570	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1629
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1630	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1689
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1690	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1749
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1750	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1809
Qy	1561	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1810	TGTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1869
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1870	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1929

Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1930	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1989
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	1990	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	2049
Qy	1750	CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	2050	CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2109
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	2110	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	2169
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2170	TCCCATAATCACCAAGACAAGAAGGGAGTGATTGCGGAAAGTTACCTCAAAGGCCACGAC	2229
Qy	1930	CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	2230	CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2289
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2290	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2349
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2350	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2409
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2410	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2469
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2470	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2529
Qy	2230	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG	2289
Db	2530	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG	2589
Qy	2290	CTGCAGCAGAAGCGGAAGCCGACCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2590	CTGCAGCAGAAGCGGAAGCCGACCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2649
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2409
Db	2650	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG	2709
Qy	2410	CCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATCACGCAGCAG	2469
Db	2710	CCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCTGCCCATCACGCAGCAG	2769

Qy 2470 GGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2529
 |||
 Db 2770 GGCTACCAGCATGAGTACGTGGACCAGCCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2829
 Qy 2530 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2589
 |||
 Db 2830 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2889
 Qy 2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCACAG 2649
 |||
 Db 2890 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCACAG 2949
 Qy 2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
 |||
 Db 2950 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3009
 Qy 2710 CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC 2769
 |||
 Db 3010 CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC 3069
 Qy 2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT 2829
 |||
 Db 3070 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT 3129
 Qy 2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG 2889
 |||
 Db 3130 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG 3189
 Qy 2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
 |||
 Db 3190 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3249
 Qy 2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
 |||
 Db 3250 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 3309
 Qy 3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
 |||
 Db 3310 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3369
 Qy 3070 AAGCCCAATGATGCGTGTACATAA 3093
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 Db 3370 AAGCCCAATGATGCGTGTACATAA 3393

RESULT 12

US-10-449-548-13

; Sequence 13, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRochelle, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

```
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 13
; LENGTH: 4250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (250)..(3390)
US-10-449-548-13
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Query Match          98.0%; Score 3030.4; DB 15; Length 4250;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3092; Conservative 0; Mismatches 1; Indels 51; Gaps 1;
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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
          |||
Db      250 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATGGCAACTATACAAAACAGTATCCGGTG 120
          |||
Db      310 CCAGAAGATTCTGAGCCAATCAGTATTTGCGATTGCAACTATACAAAACAGTATCCGGTG 369

Qy      121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
          |||
Db      370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy      181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
          |||
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Db	430	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	489
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	490	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	549
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAAACATAAGGATGAGTGCCACAACCTTT	360
Db	550	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAAACATAAGGATGAGTGCCACAACCTTT	609
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	420
Db	610	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACATAATGCCTTC	669
Qy	421	AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	480
Db	670	AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC	729
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	730	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	789
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	790	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	849
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660
Db	850	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	909
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	910	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	969
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	780
Db	970	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAGAAT	1029
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	840
Db	1030	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCTGAAGGCGCGC	1089
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	900
Db	1090	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCACATTCTCCAGGCAGTTACA	1149
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	1150	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	1209
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	1210	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1269
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1270	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1329

Qy	1081	G TTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1140
Db	1330	G TTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1389
Qy	1141	T CCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1390	T CCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG	1449
Qy	1201	G CAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1450	G CAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1509
Qy	1261	A CCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1510	A CCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1569
Qy	1321	G GATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1570	G GATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1629
Qy	1381	A ATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1630	A ATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1689
Qy	1441	G GAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1690	G GAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1749
Qy	1501	G TTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1750	G TTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG	1809
Qy	1561	T GTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1810	T GTAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1869
Qy	1621	G CCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1870	G CCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1929
Qy	1681	A ATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1930	A ATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1989
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	1990	C CTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	2049
Qy	1750	C CCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	2050	C CCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	2109
Qy	1810	C TGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	2110	C TGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	2169

Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	2170	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	2229
Qy	1930	CAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	2230	CAGCTGGTTCCCGTCACCCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2289
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2290	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2349
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2350	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2409
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2410	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2469
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2470	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2529
Qy	2230	AAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289
Db	2530	AAAGCAGACCAGCACCACTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2589
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2590	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2649
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2409
Db	2650	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2709
Qy	2410	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2469
Db	2710	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2769
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2529
Db	2770	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2829
Qy	2530	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2830	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2889
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	2890	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2949
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	2950	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	3009
Qy	2710	CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769

Db	3010	CTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	3069
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	2829
Db	3070	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT	3129
Qy	2830	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	2889
Db	3130	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	3189
Qy	2890	CAGAGGGTGGACTCCATCCAGGTGCACAGTCCCAGCCATCTGGCCAGGCCGTGACTGTC	2949
Db	3190	CAGAGGGTGGACTCCATCCAGGTGCACAGTCCCAGCCATCTGGCCAGGCCGTGACTGTC	3249
Qy	2950	TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3009
Db	3250	TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG	3309
Qy	3010	CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCCTTTCCACATCCATG	3069
Db	3310	CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCCTTTCCACATCCATG	3369
Qy	3070	AAGCCCAATGATGCGTGACATAA	3093
Db	3370	AAGCCCAATGATGCGTGACATAA	3393

RESULT 13

US-10-403-676-47

; Sequence 47, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.

```

; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME,
AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 47
; LENGTH: 3165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3153)
US-10-403-676-47

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Query Match          97.8%; Score 3025.8; DB 12; Length 3165;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 2; Indels 51; Gaps 1;

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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTTCACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db      13 ATGAGGTCAGAAGCCTTGCTGCTGTATTTCACTGCTACACTTTGCTGGGGCTGGTTTC 72

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
        |||
Db      73 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 132

Qy      121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
        |||
Db      133 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 192

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Qy	181	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	240
Db	193	ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT	252
Qy	241	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	300
Db	253	ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA	312
Qy	301	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	360
Db	313	CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT	372
Qy	361	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAAC TAATGCCTTC	420
Db	373	ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAAC TAATGCCTTC	432
Qy	421	AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTTCGGGGATGAATTCAGC	480
Db	433	AACCCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTTCGGGGATGAATTCAGC	492
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	540
Db	493	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA	552
Qy	541	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	553	AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	612
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660
Db	613	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	672
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	673	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	732
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	733	GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	792
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	840
Db	793	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	852
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	853	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA	912
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	960
Db	913	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC	972
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	973	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1032

Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1033	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1092
Qy	1081	G TTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1140
Db	1093	G TTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1152
Qy	1141	TCCAATGAGTTCCCTGATGATACCCTGAAC TTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1153	TCCAATGAGTTCCCTGATGATACCCTGAAC TTCATCAAGACGCACCCGCTCATGGATGAG	1212
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1213	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT	1272
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320
Db	1273	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1332
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1333	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1392
Qy	1381	AATGACAGCCTTTTCTGAGGAGATGAGTGTTTACAACCTTGAAAAATGCAGCTATGAT	1440
Db	1393	AATGACAGCCTTTTCTGAGGAGATGAGTGTTTACAACCTTGAAAAATGCAGCTATGAT	1452
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1453	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1512
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1513	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1572
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1573	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCGTATTGTGGATGGATAAAGGAAGGTGGT	1632
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1633	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1692
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1693	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1752
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	1753	CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	1812
Qy	1750	CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	1813	CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1872
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869

Db	1873	 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1932
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	1933	 TCCCATAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACCTCAAAGGCCACGAC	1992
Qy	1930	CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	1993	 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2052
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2053	 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2112
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109
Db	2113	 GTGCAGCGCAAGGAGAAGGAGCTCACCCTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2172
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2173	 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2232
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2233	 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2292
Qy	2230	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG	2289
Db	2293	 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG	2352
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2353	 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2412
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2409
Db	2413	 ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2472
Qy	2410	CCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2469
Db	2473	 CCCCTGCGGGCCTCCCCAGCCACATCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2532
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG	2529
Db	2533	 GGCTACCAGCATGAGTACGTGGACCAGCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG	2592
Qy	2530	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2593	 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2652
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	2653	 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2712
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709

Db 2713 CGGGAGGCCTCCCTGGGTCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2772

Qy 2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC 2769
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Db 2773 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC 2832

Qy 2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
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Db 2833 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2892

Qy 2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG 2889
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Db 2893 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG 2952

Qy 2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
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Db 2953 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3012

Qy 2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
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Db 3013 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 3072

Qy 3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
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Db 3073 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3132

Qy 3070 AAGCCCAATGATGCGTGTACA 3090
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Db 3133 AAGCCCAATGATGCGTGTACA 3153

RESULT 14

US-10-449-548-47

; Sequence 47, Application US/10449548

; Publication No. US20040018977A1

; GENERAL INFORMATION:

; APPLICANT: Alvarez, Enrique

; APPLICANT: Anderson, David W.

; APPLICANT: Dhanabal, Mohanraj

; APPLICANT: Khramtsov, Nikolai V.

; APPLICANT: LaRoche, William J.

; APPLICANT: Li, Li

; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME

; FILE REFERENCE: 15966-540CIP2

; CURRENT APPLICATION NUMBER: US/10/449,548

; CURRENT FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 60/234,082

; PRIOR FILING DATE: 2000-09-20

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; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 47
; LENGTH: 3165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3153)
US-10-449-548-47
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Query Match          97.8%; Score 3025.8; DB 15; Length 3165;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 2; Indels 51; Gaps 1;
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Qy      1 ATGAGGTCAGAAGCCTTGCTGCTATATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db      13 ATGAGGTCAGAAGCCTTGCTGCTGTATTTACACTGCTACACTTTGCTGGGGCTGGTTTC 72

Qy      61 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
        |||||||
Db      73 CCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAAAACAGTATCCGGTG 132

Qy     121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
        |||||||
Db     133 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 192

Qy     181 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
        |||||||
Db     193 ATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 252

Qy     241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 300
        |||||||
Db     253 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAACTGACATGGAAATCTAGA 312

Qy     301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 360
        |||||||
Db     313 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACCTTT 372

Qy     361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 420
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Db     373 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACCTAATGCCTTC 432
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Qy	421	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCGGGGATGAATTCAGC	480
Db	433	AACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCGGGGATGAATTCAGC	492
Qy	481	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGAGATGGA	540
Db	493	GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGAGATGGA	552
Qy	541	AACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	600
Db	553	AACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT	612
Qy	601	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	660
Db	613	CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAATGGTTGAAAGAACCA	672
Qy	661	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	720
Db	673	TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA	732
Qy	721	GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	780
Db	733	GTGGAGTATAACACCATGGGAAAGGTAGTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT	792
Qy	781	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	840
Db	793	GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTTCCTGAAGGCGCGC	852
Qy	841	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTATTTCAACATTCTCCAGGCAGTTACA	900
Db	853	TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTATTTCAACATTCTCCAGGCAGTTACA	912
Qy	901	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTCTACACCTTATAAC	960
Db	913	GATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTCTACACCTTATAAC	972
Qy	961	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1020
Db	973	AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT	1032
Qy	1021	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1080
Db	1033	GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA	1092
Qy	1081	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1140
Db	1093	GTTCCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAAGATATGCAACC	1152
Qy	1141	TCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACCCGCTCATGGATGAG	1200
Db	1153	TCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACCCGCTCATGGATGAG	1212
Qy	1201	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTTCCTGAGAACAATGGTCAGATACCGCCTT	1260
Db	1213	GCAGTGCCCTCCATCTTCAACAGGCCATGGTTTCCTGAGAACAATGGTCAGATACCGCCTT	1272
Qy	1261	ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1320

Db	1273	 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG	1332
Qy	1321	GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1380
Db	1333	 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA	1392
Qy	1381	AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1440
Db	1393	 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAAAATGCAGCTATGAT	1452
Qy	1441	GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1500
Db	1453	 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT	1512
Qy	1501	GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1560
Db	1513	 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTGAACGACATGGGAAG	1572
Qy	1561	TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT	1620
Db	1573	 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCGTATTGTGGATGGATAAAGGAAGGTGGT	1632
Qy	1621	GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1680
Db	1633	 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC	1692
Qy	1681	AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-----	1726
Db	1693	 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT	1752
Qy	1727	-----ATGGGCATTCCAGTTCCTCTTG	1749
Db	1753	 CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCTCTTG	1812
Qy	1750	CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1809
Db	1813	 CCCAGCACAAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG	1872
Qy	1810	CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1869
Db	1873	 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT	1932
Qy	1870	TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	1929
Db	1933	 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCTGGGAAAGTTACCTCAAAGGCCACGAC	1992
Qy	1930	CAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	1989
Db	1993	 CAGCTGGTTCCCGTCACCCTCTTGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC	2052
Qy	1990	GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2049
Db	2053	 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG	2112
Qy	2050	GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2109

Db	2113	GTGCAGCGCAAGGAGAAGGAGCTACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC	2172
Qy	2110	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2169
Db	2173	AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC	2232
Qy	2170	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2229
Db	2233	ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT	2292
Qy	2230	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2289
Db	2293	AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCAGAGTCAACCCCAACG	2352
Qy	2290	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2349
Db	2353	CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC	2412
Qy	2350	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2409
Db	2413	ATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGATTCCACGGACCTG	2472
Qy	2410	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2469
Db	2473	CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG	2532
Qy	2470	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2529
Db	2533	GGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGGCCAGATGGCGCTG	2592
Qy	2530	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2589
Db	2593	GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT	2652
Qy	2590	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2649
Db	2653	CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCAAAGTTCCACAG	2712
Qy	2650	CGGGAGGCCTCCCTGGGTCCCCCGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2709
Db	2713	CGGGAGGCCTCCCTGGGTCCCCCGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG	2772
Qy	2710	CTGGAAATGCACCACTCCTCTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2769
Db	2773	CTGGAAATGCACCACTCCTCTCTACGGGGTTGACTATAAGAGGAGCTACCCACGAAC	2832
Qy	2770	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT	2829
Db	2833	TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACACTAACTCCTCCAAT	2892
Qy	2830	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	2889
Db	2893	TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCGCCCG	2952
Qy	2890	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	2949
Db	2953	CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC	3012

Qy 2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
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 Db 3013 TCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGGGGCTGAAGCGTACG 3072
 Qy 3010 CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
 |||
 Db 3073 CCCTCGCTAAAGCCGGACGTACCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3132
 Qy 3070 AAGCCCAATGATGCGTGTACA 3090
 |||
 Db 3133 AAGCCCAATGATGCGTGTACA 3153

RESULT 15

US-10-403-676-17

; Sequence 17, Application US/10403676

; Publication No. US20040029150A1

; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: LaRochelle, William J.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Li, Li
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Reiger, Daniel
 ; APPLICANT: Rothenberg, Mark E.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE

; FILE REFERENCE: 21402-573B

; CURRENT APPLICATION NUMBER: US/10/403,676

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: 60/123,667

; PRIOR FILING DATE: 1999-03-09

; PRIOR APPLICATION NUMBER: 09/520,781

; PRIOR FILING DATE: 2000-03-08


```

; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 17
;   LENGTH: 3106
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(3106)
US-10-403-676-17

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Query Match          96.2%; Score 2975; DB 12; Length 3106;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 3039; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

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Qy      47 CTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTTCGCATGGCAACTATACAA 106
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Qy     107 AACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC 166
      | | | | |
Db     63 AACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC 122

Qy     167 TGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATA 226
      | | | | |
Db     123 TGGACATCCAGATGATTATGATCATGAACGGAACCCCTCTACATTGCTGCTAGGGACCATA 182

Qy     227 TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGA 286
      | | | | |
Db     183 TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGA 242

Qy     287 CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG 346
      | | | | |
Db     243 CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG 302

Qy     347 AGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTG 406
      | | | | |
Db     303 AGTGCCACAACCTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTG 362

Qy     407 GAACTAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCG 466

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Db	363	 GAACTAATGCCTTCAACCCTTCCTGCAGAACTATAAGATGGATACATTGGAACCATTTCG	422
Qy	467	GGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC	526
Db	423	 GGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC	482
Qy	527	TGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG	586
Db	483	 TGTTTGCAGATGGAAAACATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG	542
Qy	587	TCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAAT	646
Db	543	 TCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAAT	602
Qy	647	GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT	706
Db	603	 GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT	662
Qy	707	TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC	766
Db	663	 TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC	722
Qy	767	AGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGT	826
Db	723	 AGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGT	782
Qy	827	TCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTC	886
Db	783	 TCCTGAAGGCGCGCTTGAAGTCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTC	842
Qy	887	TCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTT	946
Db	843	 TCCAGGCAGTTACAGATGTGATTTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTT	902
Qy	947	CTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTG	1006
Db	903	 CTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTG	962
Qy	1007	CCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAG	1066
Db	963	 CCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAG	1022
Qy	1067	TTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAG	1126
Db	1023	 TTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAG	1082
Qy	1127	AAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACC	1186
Db	1083	 AAAGATATGCAACCTCCAATGAGTTCCTGATGATACCCTGAACCTCATCAAGACGCACC	1142
Qy	1187	CGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGG	1246
Db	1143	 CGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGG	1202
Qy	1247	TCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACA	1306

Db	1203	TCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACA	1262
Qy	1307	CTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAA	1366
Db	1263	CTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAA	1322
Qy	1367	ATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAA	1426
Db	1323	ATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACCTCTGAAA	1382
Qy	1427	AATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAA	1486
Db	1383	AATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAA	1442
Qy	1487	GCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTG	1546
Db	1443	GCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCTTGGCCGGTGTG	1502
Qy	1547	AACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGA	1606
Db	1503	AACGACATGGGAAGTGTAACCAACCTGTATTGCCTCCAGAGACCCGTATTGTGGATGGA	1562
Qy	1607	TAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGG	1666
Db	1563	TAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGG	1622
Qy	1667	ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA	1726
Db	1623	ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA	1682
Qy	1727	-----ATGGGCATT	1735
Db	1683	ATGACATTTCAACTCCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATT	1742
Qy	1736	CCAGTTCCCTCTTGCCCAGCACACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGT	1795
Db	1743	CCAGTTCCCTCTTGCCCAGCACACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGT	1802
Qy	1796	CTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTT	1855
Db	1803	CTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTT	1862
Qy	1856	TGGGGGCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACC	1915
Db	1863	TGGGGGCAGTGTCTTCCCATAAATCACCAAGACAAGAAGGGAGTGATTTCGGGAAAGTTACC	1922
Qy	1916	TCAAAGGCCACGACCAGCTGGTTCCCGTCACCTCTTGGCCATTGCAGTCATCCTGGCTT	1975
Db	1923	TCAAAGGCCACGACCAGCTGGTTCCCGTCACCTCTTGGCCATTGCAGTCATCCTGGCTT	1982
Qy	1976	TCGTTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCA	2035
Db	1983	TCGTTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCA	2042
Qy	2036	AAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCA	2095
Db	2043	AAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCA	2102

Qy	2096	TGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGC	2155
Db	2103	TGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGC	2162
Qy	2156	CGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGG	2215
Db	2163	CGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGG	2222
Qy	2216	CCAAGATGCTCATTTAAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCCAG	2275
Db	2223	CCAAGATGCTCATTTAAAGCAGACCAGCACCTGGACCTGACGGCCCTCCCCACCCCAG	2282
Qy	2276	AGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGA	2335
Db	2283	AGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGA	2342
Qy	2336	GGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGA	2395
Db	2343	GGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCATGGGCTCCCCTGTGA	2402
Qy	2396	TTCCCACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGC	2455
Db	2403	TTCCCACGGACCTGCCCCCTGCGGGCCTCCCCAGCCACATCCCCAGCGTGGTGGTCCTGC	2462
Qy	2456	CCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGG	2515
Db	2463	CCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCCAAATGAGCGAGGTGG	2522
Qy	2516	CCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATC	2575
Db	2523	CCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATC	2582
Qy	2576	TCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCC	2635
Db	2583	TCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCC	2642
Qy	2636	CCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCG	2695
Db	2643	CCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCG	2702
Qy	2696	GTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGA	2755
Db	2703	GTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCTACGGGGTTGACTATAAGAGGA	2762
Qy	2756	GCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACA	2815
Db	2763	GCTACCCACGAACCTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAGAAACAACA	2822
Qy	2816	CTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACC	2875
Db	2823	CTAACTCCTCCAATTCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACC	2882
Qy	2876	CGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC	2935
Db	2883	CGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC	2942

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Qy      2936 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGG 2995
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2943 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACCTCACTGACAAGGTCGG 3002

Qy      2996 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 3055
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3003 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 3062

Qy      3056 TTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3090
          ||||||||||||||||||||||||||||||||
Db      3063 TTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3097

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